

QY 301 GCTGAGGACGAGCTGATTATTACTGTTGTTTATATACAAACAGTAGCAGCTTTGTTATTC 360
Db 301 GCTGAGGACGAGCTGATTATTGCTGCAGCTCATATACAGCAGCAGCAGCTCTGCTATTC 360
QY 361 GGAAGAGGACCCGGTTGACCGTCTTAGGT 390
Db 361 GCGGAGGAGCAAGCTGACCGTCTTAGGT 390

RESULT 5
HSZ85358
LOCUS HSZ85358 435 bp DNA linear PRI 06-FEB-1997
DEFINITION H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285358
VERSION 285358.1 GI:1835069
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
source
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/organism="Homo sapiens"
/isolate="donor SW"
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/map="22q11.2"
/clone="25-28SWIID60"
/cell_type="lymphocyte"
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V_region
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BASE COUNT 86 a 148 c 99 g 102 t
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Best Local Similarity 91.3%; Pred. No. 1.8e-83;
Matches 356; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 ATGGCTGGACTCTGCTCTCGTCAACCTCTCACTCAGGGCAGAGGATCTCTGGGCTCAG 60
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QY 121 TGCACCTGGAACAGGAGTACGCTTGGTGTATTAATCTCTCTGGTACCACACAC 180
Db 121 TGCACCTGGAACAGGAGTACGCTTGGTGTATTAATCTCTCTGGTACCACACAC 180
QY 181 CCAGCAAAAGCCCCAAACTCATGATTATGATGTGCTAAGCGGCGCTCAGGGGTCTCT 240
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Db 241 AATCGCTTCTCTGGCTCAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300

QY 301 GCTGAGGACGAGCTGATTATTACTGTTGTTTATATACAAACAGTAGCAGCTTTGTTATTC 360
Db 301 GCTGAGGACGAGCTGATTATTACTGAGCTCATATACAGCAGCAGCAGCTCTGCTATTC 360
QY 361 GGAAGAGGACCCGGTTGACCGTCTTAGGT 390
Db 361 GGAAGTGGACCAAGGTAACCGTCTTAGGT 390

RESULT 6
HSZ85035
LOCUS HSZ85035 435 bp DNA linear PRI 06-FEB-1997
DEFINITION H.sapiens Ig lambda light chain variable region gene
(24-09ITIIIC195) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285035
VERSION 285035.1 GI:1834746
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol.
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
source
1..435
/organism="Homo sapiens"
/isolate="donor IT"
/db_xref="taxon:9606"
/map="22q11.2"
/clone="24-09ITIIIC195"
/cell_type="lymphocyte"
/tissue_type="peripheral blood"
/clone_lib="cDNA library"
/rearranged
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/gene="IGLV"
V_region
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/gene="IGLV"

BASE COUNT 85 a 149 c 102 g 99 t
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Best Local Similarity 91.0%; Pred. No. 5.2e-83;
Matches 355; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 ATGGCTGGACTCTGCTCTCGTCAACCTCTCACTCAGGGCAGAGGATCTGGGCTCAG 60
Db 1 ATGGCTGGGCTCTGCTCTCTCACTCAGGGCAGAGGCTCTGGGCCAG 60
QY 61 TCTGCCCGACTCAGGCTCCCTCTGTGTCTGGGTCTCTTGAGACAGTGGTCAACATCTCC 120
Db 61 TCTGCCCTGACTCAGGCTCCCTCGGTCTGGGTCTCTTGAGACAGTGGTCAACATCTCC 120
QY 121 TGCACCTGGAACAGGAGTACGCTTGGTGTATTAATCTCTCTGGTACCACACAC 180
Db 121 TGCACCTGGAACAGGAGTACGCTTGGTGTATTAATCTCTCTGGTACCACACAC 180
QY 181 CCAGCAAAAGCCCCAAACTCATGATTATGATGTGCTAAGCGGCGCTCAGGGGTCTCT 240
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QY 241 GATCGCTTCTCTGGCTCAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300
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Db 241 ATATCGTCTCTGGTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300
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QY 301 GCTGAGGACGAGGCTGATTATTTACTGTTTCTATATACCAACAGTAGCATCTTTGTTATTC 360
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Db 301 GCTGAGGACGAGGCTGATTATTTACTGCGAGTCTATATACCAAGCAGCAGCACTCTCTGCTTC 360
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QY 361 GGAAGAGGGACCGGTTGACCTCTCTAGGT 390
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Db 361 GGAAGAGGGACCGGTTGACCTCTCTAGGT 390
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RESULT 9

AX379222
LOCUS AX379222 605 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 264 from Patent W00196389.
ACCESSION AX379222
VERSION AX379222.1 GI:19575062
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.
Meagher, M.J., King, G.E., Xu, J. and Secrist, H.

JOURNAL Compositions and methods for the therapy and diagnosis of colon
Cancer

PATENT: WO 0196389-A 264 20-DEC-2001;
CORIXA CORPORATION (US)

LOCATION/Qualifiers
1. .605

/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 123 a 198 c 154 g 128 t 2 others

Query Match 85.6%; Score 334; DB 6; Length 605;

Best Local Similarity 91.0%; Pred. No. 5.1e-83;

Matches 355; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTCTGCTACCTCTCTCACTCAGGGCACAGGATCTCTGGGCTCAG 60

Db 33 ATGGCTGGGCTCTGCTATTTCTCACTCAGGGCACAGGGTCTCTGGGCTCAG 92

QY 61 TCTGCCCGACTCAGCTCCCTCTGCTGGGTCTCTGGACAGTCTGGTACCATCTCC 120

Db 93 TCTGCCCTGACTCAGCTCCCTCTGGGTCTCTGGACAGTCTGGTACCATCTCC 152

QY 121 TGCACTGGAAACAGGATGACCTTGGTGGTTATTAATCTATGCTCTCTGGTACCAACACAC 180

Db 153 TGCACTGGAAACAGGATGACCTTGGTGGTTATTAATCTATGCTCTCTGGTACCAACAC 212

QY 181 CCAGGCAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGGTCTCT 240

Db 213 CCAGGCAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGGTCTCT 272

QY 241 GATCGTCTCTGGTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300

Db 273 AATCGTCTCTGGTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 332

QY 301 GCTGAGGACGAGGCTGATTATTTACTGTTTCTATATACCAACAGTAGCATCTTTGTTATTC 360

Db 333 GCTGAGGACGAGGCTGATTATTTACTGCGAGTCTATATAGCATCATCACTGTGTGTTTC 392

QY 361 GGAAGAGGGACCGGTTGACCTCTCTAGGT 390

Db 393 GCGGAGGGACCAAGGTGACCTCTCTAGGT 422

RESULT 10

HS285038
LOCUS HS285038 435 bp DNA linear PRI 06-FEB-1997

DEFINITION

H.sapiens Ig lambda light chain variable region gene

(24-121TIIIE213) rearranged; Ig-Light-Lambda; VLambda.

ACCESSION

Z85038

VERSION

Z85038.1 GI:1834749

KEYWORDS

antigen receptor; immunoglobulin; immunoglobulin light chain;

immunoglobulin superfamily; rearranged; variable region.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.

1 (bases 1 to 435)

Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G.

XXIX The Creation of Diversity in the Human Immunoglobulin V Lambda

Repertoire

J. Mol. Biol.

2 (bases 1 to 435)

Ignatovich, O.

Direct Submission

Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein

Engineering, Hills Road, Cambridge CB2 2QH, UK

Location/Qualifiers

1. .435

/organism="Homo sapiens"

/isolate="donor IT"

/db_xref="taxon:9606"

/map="22q11.2"

/clone="24-121TIIIE213"

/cell_type="lymphocyte"

/tissue_type="peripheral blood"

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1. .435

/gene="IGLV"

1. .435

/gene="IGLV"

BASE COUNT 78 a 154 c 107 g 96 t

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Query Match 84.8%; Score 330.8; DB 9; Length 435;

Best Local Similarity 90.5%; Pred. No. 4.1e-82;

Matches 353; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTCTGCTCAGCTCTCTCACTCAGGGCACAGGATCTCTGGGCTCAG 60

Db 1 ATGGCTGGGCTCTGCTCTCTCTCACTCAGGGCACAGGATCTCTGGGCTCAG 60

QY 61 TCTGCCCGACTCAGCTCCCTCTGCTGGGTCTCTGGACAGTCTGGTACCATCTCC 120

Db 61 TCTGCCCTGACTCAGCTCCCTCTGGGTCTCTGGACAGTCTGGTACCATCTCC 120

QY 121 TGCACTGGAAACAGGATGACCTTGGTGGTTATTAATCTATGCTCTCTGGTACCAACACAC 180

Db 121 TGCACTGGAAACAGGATGACCTTGGTGGTTATTAATCTATGCTCTCTGGTACCAACAC 180

QY 181 CCAGGCAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGGTCTCT 240

Db 181 CCAGGCAAGCCCAAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGGTCTCT 240

QY 241 GATCGTCTCTGGTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300

Db 241 GATCGTCTCTGGTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300

QY 301 GCTGAGGACGAGGCTGATTATTTACTGTTTCTATATACCAACAGTAGCATCTTTGTTATTC 360

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QY 361 GGAAGAGGGACCGGTTGACCTCTCTAGGT 390

Db 361 GCGGAGGGACCAAGGTGACCTCTCTAGGT 390

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 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 200 a 283 c 219 g 178 t

Query Match 86.9%; Score 338.8; DB 12; Length 880;
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 Matches 358; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 1 ATGGCTGGACTCTGCTCTCTGTCACCTCTCTCACTCAGGGCACAGGATCTTGGGCTCAG 60
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 QY 61 TCTGCCCCGACTCAGCTCCCTCTGCTGCTGGTCTCTGGACAGTCTGGTCAACATCTCC 120
 DB 93 TCTGCCCCGACTCAGCTCCCTCTGCTGCTGGTCTCTGGACAGTCTGGTCAACATCTCC 152
 QY 121 TGCACCTGGAACACGAGGATGACCTTGGTGGTTATTAATCTATGCTCTGGTACCAACACAC 180
 DB 153 TGCACCTGGAACACGAGGATGACCTTGGTGGTTATTAATCTATGCTCTGGTACCAACAC 212
 QY 181 CCAGGAAAGCCGCCAACTATGATTTATGATGTCGTAAGCGGGCTCAGGGTCTCT 240
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 DB 273 AATCGCTTCTCTGGTCCAAAGTCTGGACACGGCTCCCTGACCATCTCTGGGCTCCAG 332
 QY 301 GCTGAGGACGAGGCTGATTTACTGTTGTTTATATACCAACAGTAGCATTGTTGTTATTC 360
 DB 333 GCTGAGGACGAGGCTGATTTACTGACGCTCATATACAGCAGGACGACTGTGGTATTC 392
 QY 361 GGAAGAGGACCGGTTGACCGTCTTAGGT 390
 DB 393 GCGGGAGGACCAAGTGACCGTCTTAGGT 422

RESULT 2
 BG756493
 LOCUS 843 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602715633F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855593 5',
 mRNA sequence.
 ACCESSION BG756493
 VERSION BG756493.1 GI:14067146
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 843)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM1705 row: b column: 10
 High quality sequence stop: 838.
 Location/Qualifiers
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 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 187 a 278 c 217 g 161 t

Query Match 85.6%; Score 334; DB 12; Length 843;
 Best Local Similarity 91.0%; Pred. No. 1.2e-83;
 Matches 355; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 QY 1 ATGGCTGGACTCTGCTCTCTGTCACCTCTCTCACTCAGGGCACAGGATCTTGGGCTCAG 60
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 QY 61 TCTGCCCCGACTCAGCTCCCTCTGCTGCTGGTCTCTGGACAGTCTGGTCAACATCTCC 120
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 DB 154 TGCACCTGGAACACGAGGATGACCTTGGTGGTTATTAATCTATGCTCTGGTACCAACAC 213
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 DB 214 CCAGGACAGGCTCCAAAGTCTGGACACGGCTCCCTGACCATCTCTGGGCTCCAG 273
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 DB 394 GCGGGAGGACCAAGTGACCGTCTTAGGT 423

RESULT 3
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 DEFINITION AGENCOURT 6615290 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480018
 5', mRNA sequence.
 ACCESSION BG914350
 VERSION BG914350.1 GI:19364729
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1078)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)

LOCUS BG685732 829 bp mRNA linear EST 01-MAY-2001
DEFINITION 602637827F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765447 5',
mRNA sequence.
ACCESSION BG685732
VERSION BG685732.1 GI:13917129
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 829)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI624 row: f column: 08
High quality sequence stop: 821.
Location/Qualifiers
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/clone="IMAGE:4765447"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 185 a 279 c 214 g 151 t
ORIGIN
Query Match 84.8%; Score 330.8; DB 12; Length 829;
Best Local Similarity 90.5%; Pred.No. 9.7e-83; Mismatches 37; Indels 0; Gaps 0;
Matches 353; Conservative 0;
QY 1 ATGGGCTGGACTCTGCTCTCGTCACCCCTCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
DB 32 ATGGCTGGGCTCTGCTCTCTCACTCAGGGGCACAGGATCCTGGGCTCAG 91
QY 61 TCTGCCCGACCTCAGCTCCCTCTGTGTCTGGGTCTCTGGAGCAGTGGGTACACATCTCC 120
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QY 121 TGCACCTGGACACAGGATGACGTTGGTGGTTAATACTATGCTCTGGTACCAACACCAC 180
DB 152 TGCACCTGGACACAGGATGACGTTGGTGGTTAATACTATGCTCTGGTACCAACACCAC 211
QY 181 CCAGGCAAGCCGCCAACTCATGATTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 240
DB 212 CCAGGCAAGCCGCCAACTCATGATTATGAGTTCAGTAAAGCGGCTCAGGGGTCTCT 271
QY 241 GATCGTCTCTGGTCTCAAGTCTGGCAACACAGGCTCCCTGACCATCTCTGGGCTCAG 300
DB 272 GATCGTCTCTGGTCTCAAGTCTGGCAACACAGGCTCCCTGACCGTCTCTGGGCTCAG 331
QY 301 GCTGAGGACAGGCTGATTATTACTGTTCTATATACAAACAGTAGGACTTTGTTATTC 360
DB 332 GCTGAGGATGAGGCTGATTATTACTGACGCTCATATGACGGCAGCAACATTATGCTTTC 391

QY 361 GGAAGAGGACCCGGTTGACCGTCTTAGGT 390
DB 392 GGAAGTGGACCAAGGTCAACGTCCTTAGGT 421
RESULT 6
LOCUS BG759257 686 bp mRNA linear EST 15-MAY-2001
DEFINITION 602710936F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851128 5',
mRNA sequence.
ACCESSION BG759257
VERSION BG759257.1 GI:14069910
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 686)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI693 row: h column: 09
High quality sequence stop: 683.
Location/Qualifiers
FEATURES
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/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 151 a 230 c 177 g 128 t
ORIGIN
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Best Local Similarity 90.3%; Pred.No. 2.5e-82; Mismatches 38; Indels 0; Gaps 0;
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DB 32 ATGGCTGGGCTCTGCTCTCTCACTCAGGGGCACAGGATCCTGGGCTCAG 91
QY 61 TCTGCCCGACCTCAGCTCCCTCTGTGTCTGGGTCTCTGGAGCAGTGGGTACCATCTCC 120
DB 92 TCTGCCCTGACTCAGCTCCCTCCGGGTCTCTGGAGCAGTGGGTACCATCTCC 151
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DB 152 TGCACCTGGACACAGGATGACGTTGGTGGTTAATACTATGCTCTGGTACCAACACCAC 211
QY 181 CCAGGCAAGCCGCCAACTCATGATTATGATGTCGCTAAGCGGCTCAGGGGTCTCT 240
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QY 241 GATCGTCTCTGGCTCCAACTCAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCAG 300


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QY 181 CCAGGCAAGCCCAAACTCATGATTTATGATGTCGCTAAGCGGCCTCAGGGTCTCT 240
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QY 241 GATCGCTTCTCTGGTCTCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
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Db 269 AATCGCTTCTCTGGTCTCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 328
QY 301 GCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACACAGTAGACATTTGTTATTC 360
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Db 329 GCTGAGGACGAGGCTGATTTACTGCACTCATATACAAGCAGCGGCATCCCGGTGTTTC 388
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RESULT 9
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LOCUS 60271301F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853450 5',
DEFINITION mRNA sequence.
ACCESSION BG758901
VERSION BG758901.1 GI:14069554
KEYWORDS EST.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 786)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1699 row: 1 column: 03
High quality sequence stop: 786.

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/db_xref="taxon:9606"
/clone="IMAGE:4853450"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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BASE COUNT 176 a 261 c 206 g 143 t
ORIGIN

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Query Match 84.4%; Score 329.2; DB 12; Length 786;
Best Local Similarity 90.3%; Pred. No. 2.7e-82;
Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 61 TCTGCCCGACTCAGCCTCCCTCTGTGTGTGGGTCTCTCGACAGTCGGTCACCATCTCC 120
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QY 181 CCAGGCAAGCCCAAACTCATGATTTATGATGTCGCTAAGCGGCCTCAGGGTCTCT 240
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QY 241 GATCGCTTCTCTGGTCTCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
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QY 301 GCTGAGGACGAGGCTGATTTACTGTTGTTTCATATACAACAGTAGACATTTGTTATTC 360
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Db 332 GCTGAGGATGAGGCTGATTTACTGCACTCATATGCAAGCTCATATGCAAGCAGCAACAATTATGTTCTTC 391
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RESULT 10
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LOCUS 6027113662F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853919 5',
DEFINITION mRNA sequence.
ACCESSION BG756342
VERSION BG756342.1 GI:14066995
KEYWORDS EST.
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1700 row: 1 column: 16
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/clone="IMAGE:4853919"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

```

BASE COUNT 215 a 289 c 222 g 163 t
ORIGIN

```

```

Query Match 84.4%; Score 329.2; DB 12; Length 889;

```


CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 756 BP; 161 A; 240 C; 197 G; 158 T; 0 other;

Query Match 78.7%; Score 306.8; DB 23; Length 756;

Best Local Similarity 86.7%; Pred. No. 7.8e-84;

Matches 338; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTCCCTCGTCAACCTCTCCCTCACTCAGGGCAGAGGATCCTGGGCTCAG 60
DB 1 ATGGCTGGACTCTGCTATTCCTCAACCTCTCCCTCACTCAGGGCAGAGGATCCTGGGCTCAG 60
QY 61 TGTGCCCCGACTCAGCTCTCTCTGTCTGGGTCTCTGGACAGTGGTCAACATCTCC 120
DB 61 TGTGCCCCGACTCAGCTCTCTCTGTCTGGGTCTCTGGACAGTGGTCAACATCTCC 120
QY 121 TGCACCTGGAAACAGGACGATCAGCTTGGTGTATTAATATGTCTCTGGTACCAACACAC 180
DB 121 TGCATTTGGACACGACGATGACATTTGGTGTATTAATATGTCTCTGGTACCAACATAT 180
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DB 181 CCAGGCAAGACCCCAAACTCTGATTTTGTATGTCTGGTGGCGGCTCAGGGATTTCT 240
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QY 301 GCTGAGGACGAGCTGATTTATTTACTTGTCTTATATACAAACAGTAGACATTTGTTATTC 360
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QY 361 GGAAGAGGACCGGTTGACCTCTAGGT 390
DB 361 GCGGAGGACGAGCTGACCGCTCTTGGT 390

RESULT 11

AAS87037
ID AAS87037 standard; cDNA; 866 BP.

XX
AC AAS87037;

XX
DT 13-FEB-2002 (first entry)

XX
DE DNA encoding novel human diagnostic protein #22841.

XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX
OS Homo sapiens.

XX
PN WO200175067-A2.

XX
PD 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000; 2000US-0540217.

XX
PR 23-AUG-2000; 2000US-0649167.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Drmanac RT, Liu C, Tang YT;

XX
DR WPI; 2001-639162/73.
XX
PT P-PSDB; ABG222850.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
XX Claim 1; SEQ ID No 22841; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 866 BP; 200 A; 274 C; 213 G; 179 T; 0 other;

Query Match 78.7%; Score 306.8; DB 23; Length 866;

Best Local Similarity 86.7%; Pred. No. 8.2e-84;

Matches 338; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTCCCTCGTCAACCTCTCCCTCACTCAGGGCAGAGGATCCTGGGCTCAG 60
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DB 181 CCAGGCAAGACCCCAAACTCTTGAATTTTGTATGTCTGCTGGGCTCAGGGATTTCT 240
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QY 361 GGAAGAGGACCGGTTGACCGCTCTAGGT 390
DB 361 GCGGAGGACGAGCTGACCGCTCTTGGT 390

RESULT 12

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ID ABV22585 standard; cDNA; 1636 BP.

XX
XX
XX ABV22585;


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; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: CDS
; LOCATION: 1..390
;
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..390
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

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Best Local Similarity 100.0%; Pred. No. 1.7e-119;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGACACTGCTCTCTGTCACCCCTCTCACTCAGGGACAGGATCCTGGGCTCAG 60
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QY 61 TCTGCCCGACTCAGCTCCCTCTGTGTCCTGGTCTCCTGGACAGTCGGTCAACCTCTCC 120
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DB 121 TGCACCTGGAACACGAGCATGACGTGGTGGTTATTAATATGTCTCTGGTACCAACACCA 180

QY 181 CCAGGCAAAAGCCCAAACTCATGTTTATGATGTCGCTAAGGGGCTCAGGGGTCTCT 240
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QY 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300
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DB 301 GCTGAGGACGAGCTGATTATTAATGTTTATATGTTTATATATACATATACCAACAGTAGCACTTTGTTATTC 360

QY 361 GGAAGAGGACCGGTTGACCTCTAGGT 390
DB 361 GGAAGAGGACCGGTTGACCTCTAGGT 390
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RESULT 2
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; Sequence 1, Application US/09019441
; Publication No. US20030086921A1
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
;
; TITLE OF INVENTION: ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
;
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
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;
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..390
;
; NAME/KEY: mat_peptide
; LOCATION: 58..390
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-019-441-1

Query Match      100.0%; Score 390; DB 9; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.7e-119;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGACACTGCTCTCTGTCACCCCTCTCACTCAGGGACAGGATCCTGGGCTCAG 60
DB 1 ATGGCTGACACTGCTCTCTGTCACCCCTCTCACTCAGGGACAGGATCCTGGGCTCAG 60

QY 61 TCTGCCCGACTCAGCTCCCTCTGTGTCCTGGTCTCCTGGACAGTCGGTCAACCTCTCC 120
DB 61 TCTGCCCGACTCAGCTCCCTCTGTGTCCTGGTCTCCTGGACAGTCGGTCAACCTCTCC 120

QY 121 TGCACCTGGAACACGAGCATGACGTGGTGGTTATTAATATGTCTCTGGTACCAACACCA 180
DB 121 TGCACCTGGAACACGAGCATGACGTGGTGGTTATTAATATGTCTCTGGTACCAACACCA 180

QY 181 CCAGGCAAAAGCCCAAACTCATGTTTATGATGTCGCTAAGGGGCTCAGGGGTCTCT 240
DB 181 CCAGGCAAAAGCCCAAACTCATGTTTATGATGTCGCTAAGGGGCTCAGGGGTCTCT 240

QY 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300
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QY 301 GCTGAGGACGAGCTGATTATTAATGTTTATATATACATATACCAACAGTAGCACTTTGTTATTC 360
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RESULT 3
US-10-198-846-13206/c
; Sequence 13206, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; FOR IDENTIFICATION, FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
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Job time : 102.95 secs

Genome version: 5.1.6
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Without alignment
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Prod. No. is the number of results that are greater than or equal to the score and is derived by analysis of the total score distribution.

SUMMARY

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8	328	84.3	429	16	US 09 168 444
9	327	84.0	440	41	US 10 104 444
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21	324	83.2	421	16	US 09 216 444

22 324.4 83.2 421 29 US-09-737-223-16692 Sequence 16692, A
23 324.4 83.2 421 34 US-09-918-995-16692 Sequence 16692, A
24 324.4 83.2 421 35 US-09-939-397-1488 Sequence 1488, Ap
25 324.2 83.1 509 25 US-09-652-127-62 Sequence 62, Appl
26 322.8 82.8 430 17 US-09-359-067-5162 Sequence 5162, Ap
27 322.8 82.8 508 26 US-09-665-486-564 Sequence 564, App
28 322.8 82.8 508 60 US-60-168-599-294 Sequence 294, App
29 322.4 82.7 1460 1 PCT-US02-04175-8 Sequence 8, Appli
30 322.4 82.7 1460 39 US-10-076-747-8 Sequence 8, Appli
31 322.2 82.6 425 17 US-09-359-067-38195 Sequence 38195, A
32 321.2 82.4 379 18 US-09-489-036-8482 Sequence 8482, Ap
33 321.2 82.4 379 35 US-09-943-143-8482 Sequence 8482, Ap
34 321.2 82.4 862 26 US-09-665-486-563 Sequence 563, App
35 321.2 82.4 862 60 US-60-168-599-293 Sequence 293, App
36 321.2 82.4 891 14 US-09-049-672-23 Sequence 23, Appli
37 320.8 82.3 411 16 US-09-287-618-20660 Sequence 20660, A
38 320 82.1 459 16 US-09-240-371-7751 Sequence 7751, Ap
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41 320 82.1 459 34 US-09-919-724-7751 Sequence 7751, Ap
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43 319.6 81.9 451 35 US-09-933-524-70521 Sequence 70521, A
44 319.6 81.9 451 35 US-09-933-524A-70521 Sequence 70521, A
45 319.6 81.9 468 62 US-60-184-773-1603 Sequence 1603, Ap

ALIGNMENTS

RESULT 1
US-09-019-441-1
; Sequence 1, Application US/09019441
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 1..390
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..390
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-019-441-1
Query Match 100.0%; Score 390; DB 14; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.8e-101; Indels 0; Gaps 0;
Matches 390; Conservative 0; Mismatches 0;
QY 1 ATGCGCTGGACTCTGCTCCTCGTCACCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
Db 1 ATGCGCTGGACTCTGCTCCTCGTCACCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
QY 61 TCTGCCCGGACTCAGCCTCCTCTGTGTCTGGGTCTCTTGACAGTCTGGTCAACATCTCT 120
Db 61 TCTGCCCGGACTCAGCCTCCTCTGTGTCTGGGTCTCTTGACAGTCTGGTCAACATCTCT 120
QY 121 TGCACTGGAACCCAGCGATGACGTTGGTGGTTAACTATGTCCTCGTACCAACACCAC 180
Db 121 TGCACTGGAACCCAGCGATGACGTTGGTGGTTAACTATGTCCTCGTACCAACACCAC 180
QY 181 CCAGGCAAGCCCAAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
Db 181 CCAGGCAAGCCCAAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTCTCT 240
QY 241 GATCGTTCTTGCTCAAGTCTGGAACACGCGCTCCCTGACGATCTCTGGGCTCCAG 300
Db 241 GATCGTTCTTGCTCAAGTCTGGAACACGCGCTCCCTGACGATCTCTGGGCTCCAG 300
QY 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTTATATACAAACAGTACGACATTTGTTATTC 360
Db 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTTATATACAAACAGTACGACATTTGTTATTC 360

RESULT 2
US-09-292-053-1
; Sequence 1, Application US/09292053
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: NAKAMURA, TAKEHIKO
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
; THEREOF AS THERAPEUTICS
; FILE REFERENCE: 23522.0699
; CURRENT APPLICATION NUMBER: US/09/292,053
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 08/803,085
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)-(58)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(390)
; NAME/KEY: CDS
; LOCATION: (1)..(390)
US-09-292-053-1
Query Match 100.0%; Score 390; DB 16; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.8e-101; Indels 0; Gaps 0;
Matches 390; Conservative 0; Mismatches 0;

Best Local Similarity 90.0%; Pred. No. 3e-83;
Matches 351; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTCTGTCACCCCTCTCACTCAGGGGACAGGATCTCGGGCTCAG 60
Db ATGGCTGGGCTCTGCTATTCCTCACTCAGGGGACAGGCTCTCGGGCCAG 93

QY 61 TCTGCCCGACTCAGCTCCCTCTGTCCTGGGTCTCTGGACAGTCGGTCAACCATCTCC 120
Db TCTGCCCTGACTCAGGCTCCCTCTGTCCTGGGTCTCTGGACAGTCGATCAACATCTCC 153

QY 121 TGCACCTGGAACACGAGATGACGTGGTGGTTTAACTATGTCTCTGGTGTACCAACACAC 180
Db TGCACCTGGAACACGAGTGCAGTGGTGGTTTAACTATGTCTCTGGTGTACCAACACAC 213

QY 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGTCTCT 240
Db CCAGGCAAGCCCCCAACTCATGATTTATGATGTCAGTAATCGGCCCTCAGGGGTTTCA 273

QY 241 GATCGCTTCTCTGGCTCCAACTCTGGCAACAGGCTCCCTGACCATCTCTGGGTCCAG 300
Db ATCGCTTCTCTGGCTCCAACTCTGGCAACAGGCTCCCTGACCATCTCTGGGTCCAG 333

QY 301 GCTGAGGACGAGCTGATTATTAATCTGTTTATATATACAAACAGTAGCATTTGTTATTC 360
Db GCTGAGGACGAGCTGATTATTAATCTGTTTATATATACAAAGTTTCAGTACTCGGGTGTTC 393

QY 361 GGAAGAGGACCGGTTGACCGTCTTAGGT 390
Db GCGGGAGGACGAGACTGACCGTCTTAGGT 423

RESULT 10
US-10-198-846-13206/c
; Sequence 13206, Application US/10198846
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13206
; LENGTH: 1640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13206

Query Match 84.0%; Score 327.6; DB 41; Length 1640;
Best Local Similarity 90.0%; Pred. No. 3.6e-83;
Matches 351; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTCTGTCACCCCTCTCACTCAGGGGACAGGATCTCGGGCTCAG 60
Db ATGGCTGGGCTCTGCTCTCTGTCACCTCTCACTCAGGGGACAGGATCTCGGGCTCAG 1510

QY 61 TCTGCCCGACTCAGCTCCCTCTGTCCTGGGTCTCTGGACAGTCGGTCAACATCTCC 120
Db TCTGCCCTGACTCAGGCTCCCTCTGTCCTGGGTCTCTGGACAGTCGATCAACATCTCC 1450

QY 121 TGCACCTGGAACACGAGTGCAGTGGTGGTTTAACTATGTCTCTGGTGTACCAACACAC 180
Db TGCACCTGGAACACGAGTGCAGTGGTGGTTTAACTATGTCTCTGGTGTACCAACACAC 1390

QY 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGCTCTCT 240

Db CCAGGCAAGCCCCCAACTCTCATCTATGATCTCAGTAAGCGGCCCTCAGGGGTTTCT 1330

QY 241 GATCGCTTCTCTGGCTCCAACTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db AATCGCTTCTCTGGCTCCAACTCTGGCAACACGGCTCCCTGACAAATCTCTGGGCTCCAG 1270

QY 301 GCTGAGGACGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGCATTTGTTATTC 360
Db GCTGAGGATGAGGCTGATTATTAATCTGCTCATATGAGATATAGCATTTGGGTGTTTC 1210

QY 361 GGAAGAGGACCGGTTGACCGTCTTAGGT 390
Db GCGGGAGGACCAAGCTGACCGTCTTAGGT 1180

RESULT 11
US-09-359-067-41768
; Sequence 41768, Application US/09359067
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-747CON1
; CURRENT APPLICATION NUMBER: US/09/359,067
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/131,598
; EARLIER FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 49786
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41768
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-359-067-41768

Query Match 83.9%; Score 327.4; DB 17; Length 465;
Best Local Similarity 91.3%; Pred. No. 2.9e-83;
Matches 359; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 1 ATGGCTGGACTCTGCTCTCTGTCACCCCTCTCACTCAGGGGACAGGATCTCGGGCTCAG 60
Db ATGGCTGGGCTCTGCTCTCTGTCACCTCTCACTCAGGGGACAGGCTCTCGGGCCAG 114

QY 61 TCTGCCCGACTCAGCTCCCTCTGTCCTGGGTCTCTGGACAGTCGGTCAACATCTCC 120
Db TCTGCCCTGACTCAGCTCCCTCTGTCGGGTCTCTGGACAGTCGATCAACATCTCC 174

QY 121 TGCACCTGGAACACGAGGATGAGCTGGTGGTTTAACTATGTCTCTGGTGTACCAACACAC 180
Db TGCACCTGGAACACGAGTGCAGTGGTGGTTTAACTATGTCTCTGGTGTACCAACACAC 234

QY 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTAAGCGGGCTCAGGGGTTCTCT 240
Db CCAGGCAAGCCCCCAACTCATGATTTATGAGGTGAGTAATCGGCCCTCAGGGGTTCT 294

QY 241 GATCGCTTCTCTGGCTCCAACTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db AATCGTCTCTGCTCCAACTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 354

QY 301 GCTGAGGACGAGGCTGATTATTAATCTGTTTATATACAAACAGTAGGACT---TTGTTA 357
Db GCTGAGGACGAGGCTGATTATTAATCTGAGCTCATATACAGCAGGACACTCCCGTGTTA 414

QY 358 TCGGAAGAGGACCGGTTGACCGTCTTAGGT 390
Db TCGGGAGGAGCAAGCTGACCGTCTTAGGT 447

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RESULTS:
Query Match      81.0%  Score 14.41  E-01  Ident 4.0%
Best Local Similarity 80.6%  Ident 3.9%  E-01  Ident 4.0%
Matches 349; Conservative 6; Mismatches 49; Indels 0; Gaps 0

APPLICANT: HYSEQ, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: 2001/070434
CURRENT APPLICATION NUMBER: US 09/292,053
NUMBER OF SEQ ID NOS: 14094
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 14094
LENGTH: 408
TYPE: DNA
ORGANISM: Homo sapiens

Query Match      81.0%  Score 14.41  E-01  Ident 4.0%
Best Local Similarity 80.6%  Ident 3.9%  E-01  Ident 4.0%
Matches 349; Conservative 6; Mismatches 49; Indels 0; Gaps 0

APPLICANT: HYSEQ, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: 2001/070434
CURRENT APPLICATION NUMBER: US 09/292,053
NUMBER OF SEQ ID NOS: 14094
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 14094
LENGTH: 408
TYPE: DNA
ORGANISM: Homo sapiens

```

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US-09-292-053-16573
Query Match      81.0%  Score 14.41  E-01  Ident 4.0%
Best Local Similarity 80.6%  Ident 3.9%  E-01  Ident 4.0%
Matches 349; Conservative 6; Mismatches 49; Indels 0; Gaps 0

APPLICANT: HYSEQ, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: 2001/070434
CURRENT APPLICATION NUMBER: US 09/292,053
NUMBER OF SEQ ID NOS: 14094
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 14094
LENGTH: 408
TYPE: DNA
ORGANISM: Homo sapiens

US-09-292-053-16574
Query Match      81.0%  Score 14.41  E-01  Ident 4.0%
Best Local Similarity 80.6%  Ident 3.9%  E-01  Ident 4.0%
Matches 349; Conservative 6; Mismatches 49; Indels 0; Gaps 0

APPLICANT: HYSEQ, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: 2001/070434
CURRENT APPLICATION NUMBER: US 09/292,053
NUMBER OF SEQ ID NOS: 14094
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 14094
LENGTH: 408
TYPE: DNA
ORGANISM: Homo sapiens

```

QY 241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
|||
Db 259 ATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 318
QY 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTTATATACAAACAGTAGCATTGTTATTTC 360
|||
Db 319 GCTGAGGACGAGGCTGATTATTACTGTTGTTTATATACAAACAGTAGCATTGTTATTTC 378
QY 361 CGAAGAGGACCGGTTGACCGTCTCTAGGT 390
|||
Db 379 CGAAATGGGGCCCAAGGTACCGTCTCTATGT 408

RESULT 15

US-09-332-782-36573
; Sequence 36573, Application US/09332782A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/332,782A
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36573
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-782-36573

Query Match 83.2%; Score 324.4; DB 17; Length 408;
Best Local Similarity 89.5%; Pred No. 2e-82;
Matches 349; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
QY 1 ATGGCTTGACTCTGCTCTCTGCTCACCCTCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
Db 19 ATGGCTTGGGCTCTGCTCTCTCCTCACCCTCTCACTCAGGGCACAGGCTCTGGGCCAG 78
QY 61 TCTGCCCGACTCAGGCTCCCTCTGTGTGGGTCTCTGGGACAGTGGTCACCATCTCC 120
Db 79 TCTGCCCTGACTCAGGCTCCCTCGGTCTGGGTCTCTGGGACAGTGGTCACCATCTCC 138
QY 121 TGCACCTGGAACACGAGGATGACGTTGGTGTATTAATCTCTCTGGTACCAACACAC 180
Db 139 TGCACCTGGAACACGAGGATGACGTTGGTGTATTAATCTCTCTGGTACCAACACAC 198
QY 181 CCAGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGCTCAGGGGTCTCT 240
Db 199 CCAGCAAGCCCCCAACTCATGATTTATGAGGTGAGTAAATCGGCTCAGGGGTCTCT 258
QY 241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 259 AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 318
QY 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTTATATACAAACAGTAGCATTGTTATTTC 360
Db 319 GCTGAGGACGAGGCTGATTATTACTGTTGTTTATATACAAACAGTAGCATTGTTATTTC 378
QY 361 CGAAGAGGACCGGTTGACCGTCTCTAGGT 390
Db 379 CGAAATGGGGCCCAAGGTACCGTCTCTATGT 408

Search completed: July 15, 2003, 11:45:55
Job time : 1532.5 secs

Db 289 GATCGCTTCTCTGGCTTCCAAAGTCTGGCAACACGGCTCCTGACCATTCTCTGGGCTCCAG 348
QY 301 GCTGAGGACGAGCTGATTATTACTGTTGTTTCATATACAAACAGTAGCACTTT 353
Db 349 GCTGAGGATGAGCTGATTATTACTGCTCTCATATGACGAGCTACACTTT 401

RESULT 7

US-10-310-673-1183
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo
; APPLICANT: Escobedo, Jaime
; APPLICANT: Lamson, George
; APPLICANT: Randazzo, Filippo
; APPLICANT: Moler, Edward
; APPLICANT: Klingner, Julie
; APPLICANT: Janatpour, Mary Jo
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 18095.002
; CURRENT APPLICATION NUMBER: US/10/310,673
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/336,613
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1183
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-673-1183

Query Match 79.8%; Score 311.4; DB 14; Length 562;
Best Local Similarity 88.8%; Pred. No. 6.6e-83;
Matches 349; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 1 ATGGCTTGACTCTGCTCTGCTCCTGCTCCTCCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
Db 25 ATGGCTTGGCTCTGCTATTCTCCTCCTCCTCACTCAGGCGACAGGCTCCTGGGCCAG 84
QY 61 TCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCTGGTACCATCTCC 120
Db 85 TCTGCCCTGACTCAGCCTCCCTGCTGTCTGGGTCTCTGGACAGTCTGGTACCATCTCC 144
QY 121 TGCCTGGAACGACGATGACCTTGTGTTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 240
Db 145 TGCCTGGATTCATGATGACGTTGGTGTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 264
QY 181 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 240
Db 205 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 264
QY 241 GATCGCTTCTGTGCTTCCAAAGTCTGGCAACACGGCTCCTGACCATCTCTGGGCTCCAG 300
Db 265 AGTCGCTTCTGTGGTCTCCAAAGTCTGGCAACACGGCTCCTGACCATCTCTGGGCTCCAG 324
QY 301 GCTGAGGACGAGCTGATTATTACTGTTGTTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 357
Db 325 GCTGAGGACGAGCTGATTATTATTGTCAGTTTATTTTTCAGGCGAGGCTCTCTGGGCTA 384
QY 358 TTGCGAAGAGGACCGGTTGACCGTCTTAGGT 390
Db 385 TTGCGGAGGAGGACCAAGCTGACCGTCTTAGGT 417

RESULT 8

US-60-475-872-1675
; Sequence 1675, Application US/60475872
; GENERAL INFORMATION:
; APPLICANT: Randazzo, F. et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 18095.002
; CURRENT APPLICATION NUMBER: US/10/310,673
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/336,613
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1183
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-673-1183

; FILE REFERENCE: 18376.001
; CURRENT APPLICATION NUMBER: US/60/475,872
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 9672
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1675
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-475-872-1675

Query Match 79.8%; Score 311.4; DB 20; Length 562;
Best Local Similarity 88.8%; Pred. No. 6.6e-83;
Matches 349; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
QY 1 ATGGCTTGACTCTGCTCTGCTCCTGCTCCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
Db 25 ATGGCTTGGCTCTGCTATTCTCCTCCTCCTCACTCAGGCGACAGGCTCCTGGGCCAG 84
QY 61 TCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCTGGTACCATCTCC 120
Db 85 TCTGCCCTGACTCAGCCTGCTGCTGTCTGGGTCTCTGGACAGTCTGATCACCATTCTCC 144
QY 121 TGCCTGGAACGACGATGACGTTGTTGTTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 240
Db 145 TGCCTGGATTCATGATGACGTTGGTGTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 264
QY 181 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 240
Db 205 CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 264
QY 241 GATCGCTTCTGTGCTCCTCAAGTCTGGCAACACGGCTCCTGACCATCTCTGGGCTCCAG 300
Db 265 AGTCGCTTCTGTGCTCCTCAAGTCTGGCAACACGGCTCCTGACCATCTCTGGGCTCCAG 324
QY 301 GCTGAGGACGAGCTGATTATTACTGTTGTTTATGATGTCGTTAAGCGGCTCAGGGGTCTCT 357
Db 325 GCTGAGGACGAGCTGATTATTATTGTCAGTTTATTTTTCAGGCGAGGCTCTCTGGGCTA 384
QY 358 TTGCGAAGAGGACCGGTTGACCGTCTTAGGT 390
Db 385 TTGCGGAGGAGGACCAAGCTGACCGTCTTAGGT 417

RESULT 9

US-10-170-235-35247
; Sequence 35247, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 35247
; LENGTH: 533
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-35247

Query Match 79.4%; Score 309.8; DB 15; Length 533;
Best Local Similarity 92.4%; Pred. No. 2e-82;
Matches 326; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 ATGGCTTGACTCTGCTCTGCTCCTGCTCCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
Db 34 ATGGCTTGGGCTCTGCTCCTCCTCCTCACTCAGGCGACAGGATCCTGGGCTCAG 93
QY 61 TCTGCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCTGGTACCATCTCC 120
Db 94 TCTGCCCTGACTCAGCCTCCCTCCTGTCGGGTCTCTCTGGACAGTCTGATCACCATTCTCC 153


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; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28418
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-28418

Query Match      78.3%; Score 305.4; DB 13; Length 1636;
Best Local Similarity 89.2%; Pred. No. 5.6e-81;
Matches 354; Conservative 0; Mismatches 36; Indels 7; Gaps 2;

Qy 1 ATGGCTGGACTCTGCTCTCGTCACCCCTCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
Db 60 ATGGCTGGGCTCTGCTGCTCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 119
Qy 61 TCTGCCCGACTCAGGCTCCCTCTGTGCTGGGTCTCTGGACAGTCGGTCAACATCTCC 120
Db 120 TCTGCCCTGACTCAGGCTCCCTCGTGTCTGGGTCTCTTGGACAGTCGATCAACATCTCC 179
Qy 121 TGCACCTGGAACACGAGTACGCTGTGGTGTATAA-CTATGCTCTCTGTACCAACACA 179
Db 180 TGCACCTGGAACACGAGTACGCTGTGGGTGTATAA-CTATGCTCTCTGTACCAACACA 239
Qy 180 CCCAGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTC 239
Db 240 CCCAGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTC 299
Qy 240 TGATGCTTCTCTGGCTCAAGTCTGGCAACAGGCTCCCTGACATCTCTGGGCTCA 299
Db 300 TAATGCTTCTCTGGCTCAAGTCTGGCAACAGGCTCCCTGACATCTCTGGGCTCA 359
Qy 300 GCTGAGGACGAGGTGATTTACTGTTGTTTCATATACCAACAGTAGCACT-----TT 353
Db 360 GCTGAGGACGAGGTGATTTACTGTTGTTTCATATACCAACAGTAGCACT-----TT 419
Qy 354 GTTATTGGAAGAGGACCGGTTGACCGTCTAGGT 390
Db 420 TGTCTTGGAACTGGGACCAAGGTACCGTCTAGGT 456

RESULT 13
US-10-310-673-629
; Sequence 629, Application US/10310673
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo
; APPLICANT: Escobedo, Jaime
; APPLICANT: Lamson, George
; APPLICANT: Randazzo, Filippo
; APPLICANT: Moler, Edward
; APPLICANT: Klinger, Julie
; APPLICANT: Janatpour, Mary Jo
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE OF INVENTION: IN CANCEROUS PROSTATE CELLS AND THEIR METHODS OF USE
; FILE REFERENCE: 18095.002
; CURRENT APPLICATION NUMBER: US/10/310,673
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/336,613
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: FastSeq for Windows Version 4.0
```

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; SEQ ID NO 629
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-673-629

Query Match      78.3%; Score 305.2; DB 14; Length 405;
Best Local Similarity 92.0%; Pred. No. 4.3e-81;
Matches 322; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGGCTGGACTCTGCTCTCGTCACCCCTCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
Db 40 ATGGCTGGGCTCTGCTCTCGTCACCCCTCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 99
Qy 61 TCTGCCCGACTCAGGCTCCCTCTGTGCTGGGTCTCTTGACAGTCGGTCAACATCTCC 120
Db 100 TCTGCCCTGACTCAGGCTCGCTCAGTGTCCGGGTCTCTTGACAGGAGTCACCATCTCC 159
Qy 121 TGCACCTGGAACACGAGTACGCTTGGTGGTTATAA-CTATGCTCTCTGTACCAACACA 180
Db 160 TGCACCTGGAACACGAGTACGCTTGGTGGTTATAA-CTATGCTCTCTGTACCAACACA 219
Qy 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTCT 240
Db 220 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTAAGCGGGCTCAGGGGTCTCT 279
Qy 241 GATCGCTTCTGCTGCTCCAAAGTCTGGCAACAGGCTCCCTGACATCTCTGGGCTCCAG 300
Db 280 GATCGCTTCTGCTGCTCCAAAGTCTGGCAACAGGCTCCCTGACATCTCTGGGCTCCAG 339
Qy 301 GCTGAGGACGAGGTGATTTACTGTTGTTTCATATACCAACAGTAGCAC 350
Db 340 GCTGAGGACGAGGTGATTTACTGTTGTTTCATATACCAACAGTAGCAC 389

RESULT 14
US-60-475-872-552
; Sequence 552, Application US/60475872
; GENERAL INFORMATION:
; APPLICANT: Randazzo, F. et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE OF INVENTION: IN CANCEROUS COLON CELLS AND THEIR METHODS OF USE II
; FILE REFERENCE: 18376.001
; CURRENT APPLICATION NUMBER: US/60/475,872
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 9672
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 552
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-475-872-552

Query Match      78.3%; Score 305.2; DB 20; Length 405;
Best Local Similarity 92.0%; Pred. No. 4.3e-81;
Matches 322; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 1 ATGGCTGGACTCTGCTCTCGTCACCCCTCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
Db 40 ATGGCTGGGCTCTGCTCTCGTCACCCCTCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 99
Qy 61 TCTGCCCGACTCAGGCTCCCTCTGTGCTGGGTCTCTTGACAGTCGGTCAACATCTCC 120
Db 100 TCTGCCCTGACTCAGGCTCGCTCAGTGTCCGGGTCTCTTGACAGGAGTCACCATCTCC 159
Qy 121 TGCACCTGGAACACGAGTACGCTTGGTGGTTATAA-CTATGCTCTCTGTACCAACACA 180
Db 160 TGCACCTGGAACACGAGTACGCTTGGTGGTTATAA-CTATGCTCTCTGTACCAACACA 219
Qy 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTGCTAAGCGGGCTCAGGGGTCTCT 240
Db 220 CCAGGCAAGCCCCCAACTCATGATTTATGATGCTAAGCGGGCTCAGGGGTCTCT 279
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APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1C/2D
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
US-08-958-201-13

Query Match 70.6%; Score 275.4; DB 2; Length 333;
Best Local Similarity 89.2%; Pred. No. 1.8e-72;
Matches 297; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 58 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTCGGTCACCATC 117
DB 1 CAGTCTGCTGACTCAGCCTCGCTCTGTCTGGTCTCTGGACAGTCGATCACCATC 60
QY 118 TCCTGCACCTGGAACACGAGTCGATGCTGTGGTTTAACTATGTCCTCTGGTACCAACAC 177
DB 61 TCCTGCACCTGGAACACGAGTCGATGCTGTGGTTTAACTATGTCCTCTGGTACCAACAG 120
QY 178 CACCAGGCAAGCCGCCAACTCATGATGTCGCTAAAGCGGCTCAGGGGTC 237
DB 121 CACCAGGCAAGCCGCCAACTCATGATGTCGCTAAAGCGGCTCAGGGGTT 180
QY 238 TGTGATCGCTTCTGTGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 297
DB 181 CTTAATCGCTTCTGAGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
QY 298 CAGGCTGAGGACGAGCTGATTATTACTGTTTCATATACACAGTAGCATTGTTTA 357
DB 241 CAGGCTGAGGACGAGCTGATTATTACTGAGCTCACTTACACGAGAGTCACTGTGATC 300
QY 358 TTCGGAAGAGGACCGGTTGACCGTCTAGGT 390
DB 301 TTCGGCGAGGACCAAGCTGACCGTCTTAGGT 333

RESULT 6
US-08-958-201-11
Sequence 11, Application US/08958201
Patent No. 5977319
GENERAL INFORMATION:
APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897

FILING DATE: 21-OCT-1996
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: D12 (light chain)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
US-08-958-201-11

Query Match 70.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 5.5e-72;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 58 CAGTCTGCCCGACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTCGGTCACCATC 117
DB 1 CAGTCTGCTGACTCAGCCTCGCTCTGTCTGGTCTCTGGACAGTCGATCACCATC 60
QY 118 TCCTGCACCTGGAACACGAGTCGATGCTGTGGTTTAACTATGTCCTCTGGTACCAACAC 177
DB 61 TCCTGCACCTGGAACACGAGTCGATGCTGTGGTTTAACTATGTCCTCTGGTACCAACAG 120
QY 178 CACCAGGCAAGCCGCCAACTCATGATGTCGCTAAAGCGGCTCAGGGGTC 237
DB 121 CACCAGGCAAGCCGCCAACTCATGATGTCGCTAAAGCGGCTCAGGGGTT 180
QY 238 TGTGATCGCTTCTGTGCTCCAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGTC 297
DB 181 CTTAATCGCTTCTGAGCTCCAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGTC 240
QY 298 CAGGCTGAGGACGAGCTGATTATTACTGTTTCATATACACAGTAGCATTGTTTA 357
DB 241 CAGGCTGAGGACGAGCTGATTATTACTGAGCTCACTTACACGAGAGTCACTGTGATC 300
QY 358 TTCGGAAGAGGACCGGTTGACCGTCTAGGT 390
DB 301 TTCGGCGAGGACCAAGCTGACCGTCTTAGGT 333

RESULT 7
US-09-240-274-137
Sequence 137, Application US/09240274
Patent No. 625455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 137
LENGTH: 324
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain R01
US-09-240-274-137

Query Match 61.4%; Score 239.6; DB 4; Length 324;
Best Local Similarity 86.8%; Pred. No. 7e-62;
Matches 276; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 70 ACTCAGCCTCCCTCTGTGTCCTGGTCTCTGGACAGTCGGTCACCATCTCTGCACTGGA 129


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DEFINITION Macaca mulatta Ig heavy chain variable region, anti-BPG
LOCUS MMU57565 421 bp g+gc=55
KEYWORDS antibody, mRNA, partial, Ig
SOURCE Macaca mulatta
ORGANISM Macaca mulatta
REFERENCE 1. (bases 1 to 420)
AUTHORS Andris, J. S., Miller, A. B., Atchley, J. P., Cunningham, S., Blanchet, A.,
Blanchet, A., and Capra, J. D.
TITLE Variable region gene segment: characterization of the monkey
hybridomas producing human rVH4-19 and rVH4-21 antibodies
JOURNAL Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE 9736109
PUBMED 9224966
REFERENCE 2. (bases 1 to 420)
AUTHORS Andris, J. S., Miller, A. B., Atchley, J. P., Cunningham, S., Blanchet, A.,
Blanchet, A., and Capra, J. D.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-1997) to the American Journal of
University of Texas Southwestern Medical Center, Harry Hines
Bldg., Dallas, TX 75359-9140, USA
FEATURES
source
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location/Qualifiers
organism "Macaca mulatta"
db_xref="taxon:9644"
note="hybridoma 1C9"
CDS
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/product="immunoglobulin heavy chain"
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translation "MHLMPELLVAAPWLSQVLOLRSRLVKSFELSLTCAVS
VH4-19/WHMIFQPKFLEWTSITSPINHNFLSKRYTISLTSKQFSLK
1FGLTAATAVVYCARQYSSNWAYFEWLVAVLV"
BASE COUNT 80 a 124 c 121 g 35 t
ORIGIN
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QY 421 TCA 423
DB 418 TCA 420

RESULT 4
MMU57565
LOCUS
DEFINITION Macaca mulatta Ig heavy chain variable region, anti-BPG
KEYWORDS antibody, mRNA, partial, Ig
ACCESSION U57565
VERSION U57565.1
KEYWORDS Macaca mulatta
SOURCE Macaca mulatta
ORGANISM Macaca mulatta
REFERENCE 1. (bases 1 to 420)
AUTHORS Andris, J. S., Miller, A. B., Atchley, J. P., Cunningham, S., Blanchet, A.,
Blanchet, A., and Capra, J. D.
TITLE Variable region gene segment: characterization of the monkey
hybridomas producing human rVH4-19 and rVH4-21 antibodies
JOURNAL Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE 9736109
PUBMED 9224966
REFERENCE 2. (bases 1 to 420)
AUTHORS Andris, J. S., Miller, A. B., Atchley, J. P., Cunningham, S., Blanchet, A.,
Blanchet, A., and Capra, J. D.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-1997) to the American Journal of
University of Texas Southwestern Medical Center, Harry Hines
Bldg., Dallas, TX 75359-9140, USA
FEATURES
source
1..420
location/Qualifiers
organism "Macaca mulatta"
db_xref="taxon:9644"
note="hybridoma 1C9"
CDS
1..3420
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VH4-19/WHMIFQPKFLEWTSITSPINHNFLSKRYTISLTSKQFSLK
1FGLTAATAVVYCARQYSSNWAYFEWLVAVLV"
BASE COUNT 80 a 124 c 121 g 35 t
ORIGIN
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[illegible]

RESULT 9	
AF062120	
LOCUS	
DEFINITION	
ACCESSION	AF062120
VERSION	AF062120.1
KEYWORDS	GI:3170702
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 426)
JOURNAL	Wang,X. and Stollar,B.D.
MEDLINE	Immunoglobulin VH gene expression in human aging
PUBMED	Clin. Immunol. 93 (2), 132-142 (1999)
REFERENCE	2 (bases 1 to 426)
AUTHORS	Wang,X. and Stollar,B.D.
TITLE	Direct Submission
JOURNAL	Submitted (22-APR-1998) Biochemistry Department, Tufts University
	School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA

sig peptide

V_region		/genes="IGH"		58...>426		/genes="IGH"		84 a 127 c 127 g 88 t		Query Match		73.9%; Score 312.4; DB 9; Length 426;		Best Local Similarity 86.8%; Pred. No. 4.1e-74;		Matches 369; Conservative 0; Mismatches 51; Indels 6; Gaps 2;	
BASE COUNT	ORIGIN																
Qy	1	ATGAAACAC	CTGTGGT	TTCTT	CTCTCT	CTGTGG	CGCAG	CTCC	CAGATGGG	TCCTGT	TCC	CAG	60				
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Qy	61	CTGCAG	CTGCAG	AGTCGG	CGCC	CAGGAGT	GTGA	AGCCTT	CGGAG	ACCTT	GTCC	CACC	120				
Db	61	GTGCAG	CTGCAG	AGTCGG	CGCC	CAGGACT	GTGA	AGCCTT	CGGAG	ACCTT	GTCC	CACC	120				
Qy	121	TGCGCT	GTCTCT	GTGGCT	CTGT	CACAG	TAGTAA	CTTGGT	GGA	CACTGGAT	TC	CGCAG	180				
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Qy	181	CCAGGA	AGGGA	CTCGAG	TGGAT	TGGA	ACGTAT	CTCTGGT	AGTGGT	GGGGCC	CAAC	CTAC	240				
Db	181	CCAGGA	AGGGA	CTCGAG	TGGAT	TGGA	AGCATA	CTTGGT	AGTGGT	GGGGCC	CAAC	CTAC	237				
Qy	241	ACCCCT	GTCC	TC	CAAGAG	TCGAG	TCA	TCTT	CAACAG	CACAGCT	CC	AGAAC	300				
Db	238	AACCCG	TCCT	CAAGAG	TCGAG	TCA	TCTT	CAACAG	CACAGCT	CC	AGAAC	300					
Qy	301	CTGAAC	CTGAAC	TCTGTG	ACCG	CGCG	CAC	CGCCGT	GTAT	TACTGTG	CGCAG	ATTGG	360				
Db	298	CTGAAC	CTGAG	TCTGTG	ACCG	CGCG	CAC	CGCCGT	GTAT	TACTGTG	CGCAG	ATTGG	357				
Qy	361	GCCCAA	TAGT	TGGA	CAAC	AG---	CTAGG	CTTCTGGG	CC	CAGGAG	TCCTGGT	CAC	417				
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Db	418	TCCTCA	423														

RESULT 10

HSIGHXX25

LOCUS

DEFINITION

HSIGHXX25

H.sapiens mRNA for XIA IG heavy chain VDJ region (LE 4-5).

420 bp

mRNA

linear

PRI 26-JUL-1997

• **seq peptide**
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1. .57

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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/note="Vector: pYT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldio, Ph.D. and M. Bento Soares, Ph.D."
88 a 145 c 129 g 91 t

BASE COUNT 88 a 145 c 129 g 91 t

Query Match 71.3%; Score 301.6; DB 10; Length 453;
Best Local Similarity 86.9%; Pred. No. 9.1e-70;
Matches 344; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 28 CTGGTGGCAGCTCCAGATGGCTCTGTCCTCCAGCTGCAGCTGCAGAGTCGGGCCAGGA 87
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
8 CTGGTGGCAGCTCCAGATGGCTCTGTCCTCCAGGTGACGTGCAGAGTCGGGCCAGGA 67
QY 88 GTGGTGAAGCTTCGGAGACCTGTCTCCCTACCTGCGCTGTCTCTGGTGGCTCTGTACG 147
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
68 CTGGTGAAGCTTCGGAGACCTGTCTCCCTACCTGCGCTGTCTCTGGTTACTCCATCAGC 127
QY 148 AGTAGTAACCTGTGGACCTGGATTCGCCAGCCGCCAGGGAAGGAGCTGGAGTGGATTGA 207
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
128 AGTGGTTACTCTCTGGGGCTGGATCGGCAGCCGCCAGGGAAGGGGCTGGAGTGGATTGG 187
QY 208 CGTATCTCTGGTAGTGGTGGGCCACCACTACACCCGCTCCCTCAAGAGTCGAGTCATC 267
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
188 AGTATCTATCATATA---GTGGGAGCACCTACTACACCCGCTCCCTCAAGAGTCGAGTCACC 244
QY 268 ATTTCACAGACACGCTCCAGAACACAGTTCTCCCTGAACCTGAACCTCTGTGACCCCGCG 327
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
245 ATATCAGTAGACGCTCCAGAACACAGTTCTCCCTGAAGCTGAGCTCTGTGAGCCCGCA 304
QY 328 GACAGCGCGCTGTTACTGTGCGCAGAGATTGGGCCCAATAGCTGGGAACACCGTAGGC 387
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
305 GACAGCGCGCTGTTACTGTGCGCAGACATACGGGCTATATAGTGGGTACCCCTTTGAC 364
QY 388 TTCTGGGGCCAGGAGCTCTGTGTCACCGCTCCTCA 423
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
365 TACTGGGGCCAGGAACCTGTGTCACCGTCTCTCA 400

RESULT 2
BG397580
LOCUS 602438620F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565020 5',
DEFINITION mRNA sequence.
ACCESSION BG397580
VERSION BG397580
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>
Plate: LICM1281 row: g column: 05
High quality sequence stop: 827.
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/db_xref="taxon:9606"
/clone="IMAGE:4565020"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
210 a 262 c 244 g 146 t

BASE COUNT 210 a 262 c 244 g 146 t

Query Match 71.3%; Score 301.4; DB 12; Length 862;
Best Local Similarity 85.3%; Pred. No. 1.4e-69;
Matches 361; Conservative 0; Mismatches 56; Indels 6; Gaps 2;

QY 1 ATGAACACCTGTGGTCCAG 60
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23 ATGAACACCTGTGGTCAG 82
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 121 TGCCTGTCTCTGTGGCTCTGTGCAGCAGTAGTAACCTGGTGACCTGGATCCGCCAGGCC 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
143 TGCCTGTCTCTGTGGCTCTCATCAGCAGTAGTAACCTGGTGAGTTGGGTCCGCCAGGCC 202
QY 181 CCAGGGAAGGAGTCGGAGTGGAGTTGGAGTTCTCTGGTAGTGGTGGGCCACCACTAC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
203 CCAGGGAAGGAGTCGGAGTGGAGTTGGGAAATCTATCATATA---GTGGGAGCACCACTAC 259
QY 241 AACCCGTCCTCAAGAGTCGAGTCATCATTTCAACAAGACAGTCACAAGAACCACTCTCC 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
260 AACCCGTCCTCAAGAGTCGAGTCACCATATCAGTAGACAGTCCAGAACCACTCTCC 319
QY 301 CTGAACCTGAACTCTGTGACCGCCGCGACACCGCCGCTGTATTACTGTGCCAGAGATTGG 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
320 CTGAAGCTGAGCTCTGTGACCGCCGCGACACCGCCGCTGTATTACTGTGCCAG---TCTG 376
QY 361 GCCCAATAGCTGGAACAACCGCTAGGTTCTCTGGGCCAGGAGTCTCTGGTCACCGTCTCC 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
377 GGAGACATCTTACTACTACGCTATGGACGTCCTGGGGCAAGGGACACCGGTCAACCGTCTCC 436
QY 421 TCA 423
DB |||| TCA 439

RESULT 3
BG685428
LOCUS 602637281F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
DEFINITION mRNA sequence.
ACCESSION BG685428
VERSION BG685428.1 GI:13916825
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)


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Qy 365 AAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTACCGTCTCTCTCA 423
Db 377 GCAGCTGGTACCGGTGTTTCGACCCCTGGGGCCAGGACCCCTGGTCAACCGTCTCTCTCA 435

RESULT 5
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DEFINITION AGENCOURT_8485057 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301263
5', mRNA sequence.
ACCESSION BQ710876
VERSION BQ710876.1 GI:21849775
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: n column: 16
High quality sequence stop: 560.
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/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 171 a 337 c 239 g 178 t
ORIGIN
Query Match 69.7%; Score 294.8; DB 14; Length 925;
Best Local Similarity 84.0%; Pred. No. 8.3e-68;
Matches 358; Conservative 0; Mismatches 62; Indels 5; Gaps 2;
Qy 1 ATGAACACCTGTGGTTCCTCTCTCTGGTGGCAGTCCAGATGGTCTGTGCCAG 60
Db 24 ATGAAGCACCTGTGGTTCCTCTCTCTGGTGGCAGTCCAGATGGTCTGTGCCAG 83
Qy 61 CTGCAGCTCAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 84 CTGCAGCTCAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 143
Qy 121 TCGCGTGTCTCTGGTGGCTCTGTACAGCAGTAGTA---ACTGGTGGACCTGGATCCGCCAG 177
Db 144 TGCATGTCTCTGGTGGCTCCATCAGCAGTAGTAGTACTACTGGGGTGGATCCGCCAG 203
Qy 178 CCCCAGGGAAGGGACTGGAGTGGATTTGGACGTATCTCTGGTGGTGGGGCCACCAAC 237
Db 204 CCCCCAGGGAAGGGCTGGAGTGGATTTGGACGTATCTATTATA---GTGGGAGCACCTAC 260
Qy 238 TACACCCCTCTCAAGAGTCGAGTCATCAATTTACAGACACCTCCAGAACCAAGTTC 297
Db 261 TACAACCCCTCTCAAGAGTCGAGTCATCAATTTACAGACACCTCCAGAACCAAGTTC 320
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Qy 298 TCCCTGAACCTGAACCTGTGTACCGCCGACACGGCCGTGTATTACTGTGCCAGAGAT 357
Db 321 TCCCTGAAGCTGAGCTCTGTGACCGCCGACACCGGCTGTTATTACTGTGCAGCGGC 380
Qy 358 TGGGCCCAATAGCTAGCAACACGCTAGGCTTC"GGGGCCAGGGAGTCTCTGGTCAACCTC 417
Db 381 GTAGTGGTGGTAGTGAATGTACTTCGATCTCTGGGGCCGTGGCACCTCGTCACTGTC 440
Qy 418 TCCTCA 423
Db 441 TCCTCA 446

RESULT 6
BQ710000
LOCUS BQ710000 921 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8495271 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302029
5', mRNA sequence.
ACCESSION BQ710000
VERSION BQ710000.1 GI:21848899
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM9518 row: n column: 14
High quality sequence start: 10
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/clone="IMAGE:6302029"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 186 a 313 c 244 g 176 t 2 others
ORIGIN
Query Match 69.5%; Score 294; DB 14; Length 921;
Best Local Similarity 84.4%; Pred. No. 1.4e-67;
Matches 356; Conservative 0; Mismatches 60; Indels 6; Gaps 2;
Qy 5 AACACCTGTGGTTCCTCTCTCTGGTGGCAGTCCAGATGGTCTGTCCAGCTGC 64
Db 17 AACACCTGTGGTTCCTCTCTCTGGTGGCAGTCCAGATGGTCTGTCCAGCTGC 76
Qy 65 AGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTGCCCTCACCTGCG 124
Db 77 AGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTGCCCTCACCTGCA 136
Qy 125 CTGTCTCTGGTGGTCTGTGTACAGCAGTAGTA---ACTGGTGGACCTGGATCCGCCGCCCC 181
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FT /tag= a
FT /product= "Heavy chain of 16C10 antibody"
XX WO200189567-A1.
XX PD 29-NOV-2001.
XX PF 22-MAY-2001; 2001WO-US16364.
XX PR 22-MAY-2000; 2000US-0576424.
XX PA (IDEC-) IDEC PHARM CORP.
XX PI Anderson DR, Hanna N, Brans P;
XX DR WPI: 2002-089895/12.
XX DR P-PSDB; AAU11646.
XX
XX Use of monoclonal antibody which specifically binds to B7.1 antigen
PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
PT treating cancer, graft-vs-host disease and autoimmune disease such as
PT allergy -
XX
XX Example 8; Fig 5b; 89pp; English.
PS
XX The present invention relates to a new use of a monoclonal antibody
CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
CC useful for treating diseases such as B cell cancer, lymphoma, a
CC cancer where B cells promote the growth and/or metastasis of tumours,
CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosis,
CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
CC or graft-vs-host disease. The antibody is useful for immunosuppression
CC in a human or animal and for treating or preventing resistance to or
CC rejection of transplanted organ or tissue for treating proliferative
CC and hyperproliferative diseases, for treating reversible obstructive
CC airways disease, intestinal inflammations and allergies e.g. Crohn's
CC disease and ulcerative colitis, food-related allergies e.g. migraine,
CC rhinitis and eczema, and other types of allergies. The present nucleic
CC acid sequence encodes the heavy chain of 16C10, a primatised antibody
CC used in the invention to induce apoptosis and inhibit production of
CC interleukin-2 (IL-2).
XX
XX Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
SQ

Query Match 74.0%; Score 313.2; DB 24; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.1e-71;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;
QY 1 ATGAACACCTGTGGTTCTTCTCTCTCTGGTGGGAGCTCCAGATGGTCTGTGCCAG 60
DB 1 ATGAACACCTGTGGTTCTTCTCTCTCTGGTGGGAGCTCCAGATGGTCTGTGCCAG 60
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DB 61 GTGCGAGTCCAGAGTTCGGGGCCAGGACTGGTGAAGCCCTTCGAGACCCCTGTCCCTCACC 120
QY 121 TGGCGTGTCTGTGGTGGTCTGTCTCAGCAGTAGTAATCTGTGGTGAACCTGCGCAGGCC 180
DB 121 TGGCGTGTCTGTGGTGGTCTGTCTCAGCAGTAGTAATCTGTGGTGAACCTGCGCAGGCC 180
QY 181 CCAGGGAAGGGAGTGGAGTGGATTCGACGTATCTCTGTGTAGTGGTGGGGCCACCAACTAC 240
DB 181 CCAGGGAAGGGAGTGGAGTGGATTCGACGTATCTCTGTGTAGTGGTGGGGCCACCAACTAC 240
QY 241 AACCCGTCTCCCTCAAGAGTCAGTCAATTCACCAAGACACGTCACCAAGACCCAGTTCTCC 300
DB 241 AACCCGTCTCCCTCAAGAGTCAGTCAATTCACCAAGACACGTCACCAAGACCCAGTTCTCC 300
QY 301 CTGAACCTGAATCTGTGACCCCGGACACGGCGGTGTATTACTGTGCCAGAGATTGG 360

DB 301 CTGAAGCTGAATCTGTATGACCCCGGACACGGCCGTGTATTACTGTGTGAGAGATCGT 360
QY 361 GCCCAATAGCTGGAACAA-----CGCTAGGCTTCTGGGGCCAGGGAGTC 405
DB 361 CTTTTTTCAGTGTGTGAATGGTTTACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420
QY 406 CTGGTCACCGTCTCTCTCA 423
DB 421 CTGGTCACCGTCTCTCTCA 438
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AAZ39331
ID AAZ39331 standard; DNA; 423 BP.
XX
XX AC AAZ39331;
XX
XX DT 15-FEB-2000 (first entry)
XX
XX DE Nucleotide sequence of Cynomolgous VH cDNA clone 2-5.
XX
XX KW Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity; ss.
XX
XX OS Macaca cynomolgus.
XX
XX PN WO9955369-A1.
XX
XX PD 04-NOV-1999.
XX
XX PF 28-APR-1999; 99WO-US09131.
XX
XX PR 28-APR-1998; 98US-0083367.
XX
XX PA (SMIK) SMITHLINE BEECHAM CORP.
XX
XX PI Taylor AH;
XX
XX DR WPI: 2000-023265/02
DR P-PSDB; AAY56663, AAY56728.
XX
XX PT Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
XX PS Example 3; Page 79; 123pp; English.
XX
XX CC The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
XX SQ Sequence 423 BP; 76 A; 125 C; 122 G; 100 T; 0 other;
Query Match 71.2%; Score 301.2; DB 21; Length 423;
Best Local Similarity 85.0%; Pred. No. 2e-68;
Matches 362; Conservative 0; Mismatches 58; Indels 6; Gaps 2;
QY 1 ATGAACACCTGTGGTTCTTCTCTCTCTGGTGGGAGTCCAGATGGTCTGTGCCAG 60
DB 1 ATGAACACCTGTGGTTCTTCTCTCTCTGGTGGGAGTCCAGATGGTCTGTGCCAG 60
QY 61 CTCGAGTTCGAGGAGTCGGGGCCAGGAGTGGTGAAGCCCTTCGAGACCCCTGTCCCTCACC 120
DB 61 GTGCGAGTTCGAGGAGTCGGGGCCAGGAGTGGTGAAGCCCTTCGAGACCCCTGTCCCTCACC 120
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CY      419 TCA 420
DB      419 TCA 420

RESULT 10
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ID      AAQ35903 standard; DNA, 423 BP.
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AC      AAQ35903;
XX
DT      08-JUN-1993 (first entry)
XX
DE      Anti-CD4 VH coding sequence.
XX
KW      PCR; amplify; clone; heavy; light; chains; variable; region; murine; lambda;
KW      immortalised B-cell; vector; TRAE 6; human; TIGR; mouse; antibody;
KW      recombinant; antibody; chimpanzee; in; A1; 11 world monkeys; sequence;
KW      immunoglobulin; therapeutic; rheumatoid arthritis; 187 SS
XX
CS      Sirian sp.
XX
PN      WO932198 A.
XX
PC      04-FEB-1993.
XX
PF      24-JUN-1992; 92WO 0506194
XX
PR      25-JUL-1991; 91US 0735064
PR      23-MAR-1992; 92US 0856281
XX
PA      (IDEC)- IDEC PHARM CORP.
XX
PI      Hackett N, Newman RA, Raab RW;
XX
DP      MP1; 1993 059720/07
DR      P-FSRB; AAR31948.
XX
PT      Recombinant antibodies including oliX and monkey portion of human
PT      human portion - used for treatment of various immune diseases,
PT      infectious diseases, AIDS, tumours, diabetes, inflammatory
PT      diseases, intestinal inflammations and allergies, etc.
XX
PS      Disclosure; Page 53-54; 92pp; English.
XX
CC      The sequences given in AAQ35903 04 encode the Sirian anti-CD4 VH and
CC      V-lambda sequences respectively. These sequences were obtained from
CC      the primer sequences given in AAQ35903 03. The replication plasmids
CC      were sequentially cloned into the vector pAR3, which contains the
CC      19S1 and human lambda constant regions. The amplified sequences were
CC      used in the production of a recombinant antibody. Recombinant
CC      human, chimpanzee or old world monkey immunoglobulin G (IgG)
CC      region and an antigen (Ag) binding portion of an old world monkey
CC      variable region, where the old world monkeys may be of any species,
CC      different. The recombinant antibody may be used as a therapeutic
CC      agent for the treatment of rheumatoid arthritis, organ and
CC      immunological disorders.
XX
SQ      Sequence 423 BP; 85 A; 122 C; 115 G; 101 T; 101

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CY      419 TCA 420
DB      419 TCA 420

RESULT 10
AAQ35903
ID      AAQ35903 standard; DNA, 423 BP.
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AC      AAQ35903;
XX
DT      08-JUN-1993 (first entry)
XX
DE      Anti-CD4 VH coding sequence.
XX
KW      PCR; amplify; clone; heavy; light; chains; variable; region; murine; lambda;
KW      immortalised B-cell; vector; TRAE 6; human; TIGR; mouse; antibody;
KW      recombinant; antibody; chimpanzee; in; A1; 11 world monkeys; sequence;
KW      immunoglobulin; therapeutic; rheumatoid arthritis; 187 SS
XX
CS      Sirian sp.
XX
PN      WO932198 A.
XX
PC      04-FEB-1993.
XX
PF      24-JUN-1992; 92WO 0506194
XX
PR      25-JUL-1991; 91US 0735064
PR      23-MAR-1992; 92US 0856281
XX
PA      (IDEC)- IDEC PHARM CORP.
XX
PI      Hackett N, Newman RA, Raab RW;
XX
DP      MP1; 1993 059720/07
DR      P-FSRB; AAR31948.
XX
PT      Recombinant antibodies including oliX and monkey portion of human
PT      human portion - used for treatment of various immune diseases,
PT      infectious diseases, AIDS, tumours, diabetes, inflammatory
PT      diseases, intestinal inflammations and allergies, etc.
XX
PS      Disclosure; Page 53-54; 92pp; English.
XX
CC      The sequences given in AAQ35903 04 encode the Sirian anti-CD4 VH and
CC      V-lambda sequences respectively. These sequences were obtained from
CC      the primer sequences given in AAQ35903 03. The replication plasmids
CC      were sequentially cloned into the vector pAR3, which contains the
CC      19S1 and human lambda constant regions. The amplified sequences were
CC      used in the production of a recombinant antibody. Recombinant
CC      human, chimpanzee or old world monkey immunoglobulin G (IgG)
CC      region and an antigen (Ag) binding portion of an old world monkey
CC      variable region, where the old world monkeys may be of any species,
CC      different. The recombinant antibody may be used as a therapeutic
CC      agent for the treatment of rheumatoid arthritis, organ and
CC      immunological disorders.
XX
SQ      Sequence 423 BP; 85 A; 122 C; 115 G; 101 T; 101

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Db 361 ATATTGAAATATCTTCACACTGGTTATTATATATCTGGGCCAGGGAGTCCTGGTCACCGTCTCC 420

Search completed: July 15, 2003, 08:27:56
Job time : 160.905 secs


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RESULT 15
US-10-073-138-2
; Sequence 2, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
; AND B7.2 CO-STIMULATORY ANTIGENS
;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/073,138
; FILING DATE: 13-Feb-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,361
; FILING DATE: 08-NOV-1996
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
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Qy	121	TGSCCTGTCTCTGTGGCTCTGTGCAGAGTAGTAACCTGGTCGACCTGGATCCGCGACGCC	180	
Db	121	TGCGTTGTCTCTGTGGCTCCTCAGCGGTTACTACTCGACTGTGATCCGCGAGACC	180	
Qy	181	CCAGGGAAGGACCTGGAGTGGATTGGACGTATCTCTGTGTGGTGGGGCCACCAACTAC	240	
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Search completed: July 15, 2003, 13:01:02
Job time : 111.492 secs

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

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441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

Results returned: 423
Without alignment: 423
441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

Results returned: 423
Without alignment: 423
441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

Results returned: 423
Without alignment: 423
441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

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441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

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441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

Results returned: 423
Without alignment: 423
441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

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Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

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441,974 Million cell updates/sec

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Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

Results returned: 423
Without alignment: 423
441,974 Million cell updates/sec

Search engine version 3.1.6
Copyright 1993-2003 Compuser Ltd.

Maximum number of results returned: 1000000

Results returned: 423
Without alignment: 423
441,974 Million cell updates/sec

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total gene distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	17	Percentile
1	423	100.0	423	14	US 09 013 411	0.0000000000
2	423	100.0	423	14	US 09 013 411	0.0000000000
3	423	100.0	423	40	US 09 013 411	0.0000000000
4	313.2	74.0	1431	11	US 09 013 411	0.0000000000
5	313.2	74.0	1431	17	US 09 013 411	0.0000000000
6	313.2	74.0	1431	19	US 09 013 411	0.0000000000
7	313.2	74.0	1431	22	US 09 013 411	0.0000000000
8	313.2	74.0	1431	29	US 09 013 411	0.0000000000
9	313.2	74.0	1431	35	US 09 013 411	0.0000000000
10	313.2	74.0	1431	38	US 09 013 411	0.0000000000
11	313.2	74.0	1431	39	US 09 013 411	0.0000000000
12	313.2	74.0	1431	40	US 09 013 411	0.0000000000
13	313.2	74.0	1431	43	US 09 013 411	0.0000000000
14	313.2	74.0	1431	681	US 09 013 411	0.0000000000
15	313.2	74.0	1431	681	US 09 013 411	0.0000000000
16	313.2	74.0	1431	541	US 09 013 411	0.0000000000
17	313.2	74.0	1431	423	US 09 013 411	0.0000000000
18	313.2	74.0	1431	423	US 09 013 411	0.0000000000
19	313.2	74.0	1431	423	US 09 013 411	0.0000000000
20	299.8	70.9	1404	23	US 09 013 411	0.0000000000
21	299.8	70.9	1404	23	US 09 013 411	0.0000000000

22	239.8	70.9	1404	23	US-09-612-914-11	Sequence 11, Appl
23	239.8	70.9	1404	23	US-09-612-914A-7	Sequence 7, Appl
24	239.8	70.9	1404	23	US-09-612-914A-9	Sequence 9, Appl
25	239.8	70.9	1404	23	US-09-612-914A-11	Sequence 11, Appl
26	239.8	70.9	1404	23	US-10-211-357-9	Sequence 7, Appl
27	239.8	70.9	1404	42	US-10-211-357-9	Sequence 9, Appl
28	239.8	70.9	1404	42	US-10-211-357-11	Sequence 11, Appl
29	239.8	70.5	420	1	PCT-US99-09131-44	Sequence 44, Appl
30	239.2	70.5	420	17	US-09-300-970A-44	Sequence 44, Appl
31	239.2	70.5	420	34	US-09-305-243-44	Sequence 44, Appl
32	239.2	70.5	423	3	US-07-735-064A-15	Sequence 15, Appl
33	239.2	70.5	423	7	US-08-379-072-15	Sequence 15, Appl
34	239.2	70.5	423	8	US-08-476-349-15	Sequence 15, Appl
35	239.2	70.5	423	32	US-09-850-168-15	Sequence 15, Appl
36	239.4	70.1	619	39	US-10-089-128-37	Sequence 37, Appl
37	239.6	70.1	619	60	US-60-168-599-505	Sequence 505, App
38	239.4	69.8	434	17	US-09-362-510-23569	Sequence 23569, A
39	239.5	69.8	434	17	US-09-362-510A-23569	Sequence 23569, A
40	239.5	69.8	434	34	US-09-904-013-23569	Sequence 23569, A
41	235.2	69.8	420	23	US-09-612-914-1	Sequence 1, Appl
42	235.2	69.8	420	23	US-09-612-914A-1	Sequence 1, Appl
43	235.2	69.8	420	42	US-10-211-357-1	Sequence 1, Appl
44	239.3	69.4	417	16	US-09-203-768A-1	Sequence 1, Appl
45	239.4	69.4	417	37	US-09-989-901-1	Sequence 1, Appl

ALIGNMENTS

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; NAME/KEY: CDS
; LOCATION: 1..423
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58_423
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-019-441-2

Query Match      100.0%; Score 423; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.3e-96;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1 ATGAAACACCTGTGGTTCTCTCTCTCTGTGTGGAGCTCCAGATGGTCTGTGTCCAG 60

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Db 61 CTGCAGCTGCAGGAGTCGGGCCCGAGGAGTGGTGAAGCCTTCGGAGACCTGTCTCCCTCACC 120

Qy 121 TGCCTCTCTCTGTGGCTCTGTCTGTGTGGAGTAGTAACCTGGTGGACCTGGATCCGCCAGCCC 180
Db 121 TGCCTCTCTCTGTGGCTCTGTCTGTGTGGAGTAGTAACCTGGTGGACCTGGATCCGCCAGCCC 180

Qy 181 CAGGGAAGGAGCTGGAGTGGATGGACGTATCTCTGTGTGTGGGCCACCAACATAC 240
Db 181 CAGGGAAGGAGCTGGAGTGGATGGACGTATCTCTGTGTGTGGGCCACCAACATAC 240

Qy 241 AACCCGTCTCTCAGAGTCGAGTCATCATTTCAAGACACGTCCAGAACCCAGTTCTCC 300
Db 241 AACCCGTCTCTCAGAGTCGAGTCATCATTTCAAGACACGTCCAGAACCCAGTTCTCC 300

Qy 301 CTGAACCTGAACCTCTGTGACCGCCCGACACGCGCGTATTACTGTGCCAGATTGG 360
Db 301 CTGAACCTGAACCTCTGTGACCGCCCGACACGCGCGTATTACTGTGCCAGATTGG 360

Qy 361 GCCAAATAGCTGGAACAAACGCTAGGCTTCTGGGCCAGGAGTCTGTGTCACTCTCC 420
Db 361 GCCAAATAGCTGGAACAAACGCTAGGCTTCTGGGCCAGGAGTCTGTGTCACTCTCC 420

Qy 421 TCA 423
Db 421 TCA 423

RESULT 2
US-09-292-053-3
; Sequence 3, Application US/09292053
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: NAKAMURA, TAKEHIKO
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
; FILE REFERENCE: 23522.0699
; CURRENT APPLICATION NUMBER: US/09/292,053
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 08/803,085
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(423)
; NAME/KEY: CDS
; LOCATION: (1)..(423)
US-09-292-053-3

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1431
US-08-746-361-6

Query Match 74.0%; Score 313.2; DB 11; Length 1431;
Best Local Similarity 84.5%; Pred. No. 9.3e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAAACACCTGTGGTTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTGCCAG 60
DB 1 ATGAAACACCTGTGGTTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTGCCAG 60

QY 61 CTGCAGCTCAGAGTCCGGGCCAGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120
DB 61 GTGCAGCTCAGAGTCCGGGCCAGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120

QY 121 TGCCTGTCTCTGTGGTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTGCCAG 180
DB 121 TGCCTGTCTCTGTGGTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTGCCAG 180

QY 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTGGTGGTGGTGGTGGTGGTGGTGG 240

QY 301 CTGAAGCTGAACCTCTGTGACCGCGGACACGGCGGTGTTACTGTGCCAGAGATTGG 360
DB 301 CTGAAGCTGAACCTCTGTGACCGCGGACACGGCGGTGTTACTGTGCCAGAGATTGG 360

QY 361 GCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGCGCAGGAGTGC 405
DB 361 CTTTTCCTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420

QY 406 CTGGTCAACCTCTCTCTCA 423
DB 421 CTGGTCAACCTCTCTCTCA 438

RESULT 5

US-09-383-916-11

; Sequence 11, Application US/09383916

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR E7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1431
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1431
US-09-383-916-11

Query Match 74.0%; Score 313.2; DB 17; Length 1431;
Best Local Similarity 84.5%; Pred. No. 9.3e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAAACACCTGTGGTTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTGCCAG 60
DB 1 ATGAAACACCTGTGGTTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTGCCAG 60

QY 61 CTGCAGCTCAGAGTCCGGGCCAGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120
DB 61 GTGCAGCTCAGAGTCCGGGCCAGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120

QY 121 TGCCTGTCTCTGTGGTCTCTCTCTGTGGGAGCTCCAGATGGTGGTGGTGGTGG 180
DB 121 TGCCTGTCTCTGTGGTCTCTCTCTGTGGGAGCTCCAGATGGTGGTGGTGG 180

QY 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 181 CCAGGGAAGGAGTGGAGTGGATTCCTGTGGTGGTGGTGGTGGTGGTGGTGG 240

QY 241 AACCCGTCCTCAAGAGTCCAGATCATTTTCAAGACACGTCCAAAGAACAGTTCTCC 300
DB 241 AACCCGTCCTCAAGAGTCCAGATCATTTTCAAGACACGTCCAAAGAACAGTTCTCC 300

QY 301 CTGACCTGACTCTGTACCGCGGACACGGCGGTGTTACTGTGCCAGAGATTGG 360
DB 301 CTGACCTGACTCTGTACCGCGGACACGGCGGTGTTACTGTGCCAGAGATTGG 360

Db 121 TGCACGTCTCTGGTGGCTC---CATCAGAGGTACTACTGAGCTGGATCCGGCAGCCC 177
QY 181 CCAGGGAAGGACTGAGTGGATTGGACGTATCTCTGTTAGTGGTGGGCCACCAACTAC 240
Db 178 CTTGGGAAGGACTGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAACTAC 234
QY 241 AACCCGTCTCCTCAAGAGTCGAGTCATCTTTTACAAAGACACGCTCCAAAGAACAGTTCTCC 300
Db 235 AACCCCTCCTCAAGAGTCGAGTCACCATATCAGTAGACACGCTCCAAAGAACAGTTCTCC 294
QY 301 CTGAACCTGAACCTCTGTGACCGCGGACACGGCGGTGTTATTACTGTGCCAGAGATTGG 360
Db 295 CTGAAGCTGAACCTCTGTGACCGCTCGCGACACGGCGGTGTTATTATTGTGCGAAGAGGG 354
QY 361 GCCCAATAGCTG---GAACAAGCTAGGCTTCTGGGCGCAGGAGTCTCTGTCTACCGTC 417
Db 355 GGCCTCTACGGTGACTACGGCTGGTTTCGCCCTCTGGGCGCAGGGAACCTCTGTCTACCGTC 414
QY 418 TCCTCA 423
Db 415 TCCTCA 420

RESULT 12

PCT-US02-38550-104

; Sequence:104, Application PC/TUS0238550

; GENERAL INFORMATION:

; APPLICANT: GUDAS, INC.

; APPLICANT: GUDAS, Jean

; APPLICANT: FOLTZ, Ian

; APPLICANT: HANDA, Masahisa

; APPLICANT: GALLO, Michael

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: AGENIX.027A

; CURRENT APPLICATION NUMBER: PCT/US02/38550

; CURRENT FILING DATE: 2002-12-02

; PRIOR APPLICATION NUMBER: US 60/337275

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 104

; LENGTH: 423

; TYPE: DNA

; ORGANISM: Homo sapiens

PCT-US02-38550-104

Query Match 67.8%; Score 287; DB 2; Length 423;
Best Local Similarity 84.4%; Pred. No. 1.1e-71;
Matches 362; Conservative 0; Mismatches 55; Indels 12; Gaps 3;

QY 1 ATGAACACCTGTGGTTCTCTCTCTGGTGGAGCTCCAGATGGTCTCTGTCCAG 60
Db 1 ATGAACACCTGTGGTTCTCTCTCTGGTGGAGCTCCAGATGGTCTCTGTCCAG 60
QY 61 CTGCAGCTCAGAGTCGGGCGCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 61 GTGCAGCTCAGAGTCGGGCGCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
QY 121 TGCCTGTCTCTGGTGGCTCTCTCAGCAGTAGTAACTGGTGACCTGGATCCGCCAGCCC 180
Db 121 TGCACGTCTCTGGTGGCTC---CATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCCC 177
QY 181 CCAGGGAAGGACTGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTAC 240
Db 178 CCAGGGAAGGACTGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAACTAC 234
QY 241 AACCCGTCTCCTCAAGAGTCGAGTCATCTTTTACAAAGACACGCTCCAAAGAACAGTTCTCC 300
Db 235 AACCCCTCCTCAAGAGTCGAGTCACCATATCAGTAGACACGCTCCAAAGAACAGTTCTCT 294
QY 301 CTGAGCTGTCTCTGGTGGCTCTCTCAGCAGTAGTAACTGGTGACCTGGATCCGCCAGCCC 180
Db 301 CTGAGCTGTCTCTGGTGGCTC---CATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCCC 177
QY 181 CCAGGGAAGGACTGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTAC 240
Db 178 CCAGGGAAGGACTGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAACTAC 234
QY 241 AACCCGTCTCCTCAAGAGTCGAGTCATCTTTTACAAAGACACGCTCCAAAGAACAGTTCTCC 300
Db 235 AACCCCTCCTCAAGAGTCGAGTCACCATATCAGTAGACACGCTCCAAAGAACAGTTCTCT 294
QY 301 CTGAACCTGAACCTCTGTGACCGCGGACACGGCGGTGTTATTACTGTGCCAGAGATTGG 360

Db 295 CTGAAGCTGAGCTCTGTGACCGCTCGGACACGCCCGTGTATTACTGTGCGAGATACC 354
QY 361 GCCCAATAGCTGA-----ACAACGCTAGGCTTCTGGGCGCAGGAGTCTCTGGTCAAC 414
Db 355 CGTACGATTTTGGAGTGGTTAGCGGTATGGACCTCTGGGCGCAAGGACCAACCGTCAAC 414
QY 415 GTCTCCTCA 423
Db 415 GTCTCCTCA 423

RESULT 13

US-10-309-762-104

; Sequence 104, Application US/10309762

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian

; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: AGENIX.027A

; CURRENT APPLICATION NUMBER: US/10/309,762

; CURRENT FILING DATE: 2002-12-02

; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 104

; LENGTH: 423

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-309-762-104

Query Match 67.8%; Score 287; DB 14; Length 423;
Best Local Similarity 84.4%; Pred. No. 1.1e-71;
Matches 362; Conservative 0; Mismatches 55; Indels 12; Gaps 3;

QY 1 ATGAACACCTGTGGTTCTCTCTCTGGTGGAGCTCCAGATGGTCTCTGTCCAG 60
Db 1 ATGAACACCTGTGGTTCTCTCTCTGGTGGAGCTCCAGATGGTCTCTGTCCAG 60
QY 61 CTGCAGCTCAGGAGTCGGGCGCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 61 GTGCAGCTCAGGAGTCGGGCGCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
QY 121 TGCCTGTCTCTGGTGGCTCTGTCAAGCAGTAGTAACTGGTGGAACCTGGATCCGCCAGCCC 180
Db 121 TGCACGTCTCTGGTGGCTC---CATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCCC 177
QY 181 CCAGGGAAGGACTGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTAC 240
Db 178 CCAGGGAAGGACTGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAACTAC 234
QY 241 AACCCGTCTCCTCAAGAGTCGAGTCATCTTTTACAAAGACACGCTCCAAAGAACAGTTCTCC 300
Db 235 AACCCCTCCTCAAGAGTCGAGTCACCATATCAGTAGACACGCTCCAAAGAACAGTTCTCT 294
QY 301 CTGAACCTGAACCTCTGTGACCGCGGACACGGCGGTGTTATTACTGTGCCAGAGATTGG 360
Db 295 CTGAAGCTGAGCTCTGTGACCGCTCGCGACACGGCGGTGTTATTACTGTGCCAGAGATACC 354
QY 361 GCCCAATAGCTGA-----ACAACGCTAGGCTTCTGGGCGCAGGAGTCTCTGGTCAAC 414
Db 355 CGTACGATTTTGGAGTGGTTAGCGGTATGGACCTCTGGGCGCAAGGACCAACCGTCAAC 414
QY 415 GTCTCCTCA 423
Db 415 GTCTCCTCA 423

RESULT 14

STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-133
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-237-15

Query Match 70.5%; Score 298.2; DB 1; Length 423;
Best Local Similarity 83.2%; Pred. No. 7.7e-78;
Matches 352; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

QY	1	ATGAAACACCTGTGGTTCTTCTCTCTGTTGGGAGCTCCAGATGGTCTGTCCTCCAG	60
DB	4	ATGAAACACCTGTGGTTCTTCTCTCTGTTGGGAGCTCCAGATGGTCTGTCCTCCAG	63
QY	61	CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC	120
DB	64	GTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC	123
QY	121	TGCGTGTCTCTGTTGGCTCTGTACAGCTAGTAACTGTGACCTGGATCGCCAGCC	180
DB	124	TGCAGTGTCTCTGTTGGCTCTGTACAGCTAGTAACTGTGACCTGGATCGCCAGCTCC	183
QY	181	CCAGGAGGAGGAGTGGAGTGGATTGGACGTATCTCTGTTAGTGGTGGGCCCCAACCTAC	240
DB	184	CCAGGAGGAGGAGTGGAGTGGATTGGACGTATCTCTGTTAGTGGTGGGCCCCAACCTAC	243
QY	241	AACCCGTCCCTCAAGAGTCGAGTCATCAFTTCACAGACACGTCCAAAGAACCACTTCTCC	300
DB	244	AATCCCTCCCTCAACAACTCGAGTCTCCATTTCAATAGACACGTCCAAAGAACCTTCTCC	303
QY	301	CTGAACCTGAACCTGTGACCCCGGACACGGCGTGTATTACTGTCCAGAGATTGG	360
DB	304	CTGAACCTGAAGTCTGTGACCCCGGACACGGCGTCTATTACTGTCCAGAGTAAT---	360
QY	361	GCCCAATAGCTGGAACACGCTAGCTTCTCGGGCCAGGGAGTCTGTGTACCGTCTCC	420
DB	361	ATATTGAATATCTTCACTGGTTATTATATCTGGGCCAGGGAGTCTGTGTACCGTCTCC	420
QY	421	TCA 423	
DB	421	TCA 423	

RESULT 9
US-08-478-039-107

Sequence 107, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Anti-CD4 VH
FEATURE:
NAME/KEY: CDS
LOCATION: 4..420
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 61..420
US-08-478-039-107

Query Match 69.8%; Score 295.2; DB 1; Length 420;
Best Local Similarity 83.1%; Pred. No. 5.7e-77;
Matches 349; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

QY	1	ATGAAACACCTGTGGTTCTTCTCTCTGTTGGGAGCTCCAGATGGTCTGTCCTCCAG	60
DB	4	ATGAAACACCTGTGGTTCTTCTCTCTGTTGGGAGCTCCAGATGGTCTGTCCTCCAG	63
QY	61	CTGCAGCTGCAGGAGTGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC	120
DB	64	GTGCAGCTGCAGGAGTGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC	123

Query Match	63.4%	Score 268	DB 2	Length 426
Best Local Similarity	81.5%	Pred. No. 4.8e-69		
Matches 352	Conservative 0	Mismatches 65	Indels 15	Gaps 3

Qy	1	ATGAACACCTGTGGTCTCTCTCCCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	60
Db	1	ATGAACATCTGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	60
Qy	61	CTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCCCTGTCCTCACC	120
Db	61	GTGCAGCTGCAGGAGTCTGGGCCAGGAGTGGTGAAGCTTCGGAGACCCCTGTCCTCACC	120
Qy	121	TGGCTGTCTCTGGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	180
Db	121	TGCACCTGTCTCTGGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	180
Qy	181	CCAGGAGGAGCTGGAGTGGATTTGACGCTATCTCTGGTAGTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	240
Db	178	CCAGGTAAGGGCTGGAGTGGATTTGAGGAAATCAATCATAGTGGAG---CACCACCTAC	234

APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-357

Query Match 62.9%; Score 266.2; DB 4; Length 403;
Best Local Similarity 82.5%; Pred. No. 1.6e-68;
Matches 349; Conservative 0; Mismatches 53; Indels 21; Gaps 3

Qy	1	ATGAACACCTGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	60
Db	1	ATGAACACCTGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	60
Qy	61	CTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCCCTGTCCTCACC	120
Db	61	GTGCAGCTGCAGGAGTGGGGGCGGAGACTCTTGAAGCTTCGGAGACCCCTGTCCTCACC	120
Qy	121	TGGCTGTCTCTGGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	180
Db	121	TGGCTGTCTATGGTGGGTCTCTCAG---TGGTACTACTGGAGCTGGATCCGCGAGGCC	177
Qy	181	CCAGGAGGAGCTGGAGTGGATTTGACGCTATCTCTGGTAGTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	240
Db	178	CCAGGTAAGGGCTGGAGTGGATTTGAGGAAATCAATCATAGTGGAG---CACCACCTAC	234

APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
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APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
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APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-357

Query Match 62.9%; Score 266.2; DB 4; Length 403;
Best Local Similarity 82.5%; Pred. No. 1.6e-68;
Matches 349; Conservative 0; Mismatches 53; Indels 21; Gaps 3

Qy	1	ATGAACACCTGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	60
Db	1	ATGAACATCTGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	60
Qy	61	CTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGACCCCTGTCCTCACC	120
Db	61	GTGCAGCTGCAGGAGTCTGGGCCAGGAGTGGTGAAGCTTCGGAGACCCCTGTCCTCACC	120
Qy	121	TGGCTGTCTCTGGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	180
Db	121	TGCACCTGTCTCTGGAGTCT---CATCAGTAGTCACTACTGGAGCTGGATCCGCGAGTCC	177
Qy	181	CCAGGAGGAGCTGGAGTGGATTTGACGCTATCTCTGGTAGTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	240
Db	178	CCAGGTAAGGGCTGGAGTGGATTTGAGGAAATCAATCATAGTGGAG---CACCACCTAC	234

APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
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FILING DATE: 03-DEC-1993
PRIORITY APPLICATION DATA:
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FILING DATE: 10-DEC-1993
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APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 357:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-357

Query Match 62.9%; Score 266.2; DB 4; Length 403;
Best Local Similarity 82.5%; Pred. No. 1.6e-68;
Matches 349; Conservative 0; Mismatches 53; Indels 21; Gaps 3

Qy	1	ATGAACACCTGTGGTCTCTCTCTCCCTGGTGGGAGCTCCAGATGGGTCTGTCCTCCAG	60
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Silverman,G.J.
Variable region gene analysis of pathologic human autoantibodies to
the related I and I red blood cell antigens
JOURNAL Blood (1991) in press
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BASE COUNT 104 a 122 c 102 g 101 t
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Query Match 88.4%; Score 342.2; DB 9; Length 429;
Best Local Similarity 92.8%; Pred. No. 1.1e-101;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 1 ATGGACATCAGGGTCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGGACATCAGGGTCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGACAGA 120
Qy 121 GTCACATCATTGTCAGGCAAGTCCAGCATATAGGTATATTAAATTGGTATCAGCAG 180
Db 121 GTCACATCATTGTCAGGCAAGTCCAGCATATAGGTATATTAAATTGGTATCAGCAG 180
Qy 181 AAACAGGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTC 240
Db 181 AAACAGGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTC 240
Qy 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCCTCAGCAGCCTG 300
Db 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCCTCAGCAGCCTG 300
Qy 301 CAGCTGAAGATTTTGCAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 301 CAGCTGAAGATTTTGCAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Qy 361 GGCCAGGACCAAGGTGGAATCAA 387
Db 361 GGCCAGGACCAAGGTGGAATCAA 387

RESULT 2
LOCUS E40896 Humanized anti-Fas antibody. 729 bp DNA linear PAT 31-JAN-2002
DEFINITION E40896
ACCESSION E40896.1 GI:18627473
VERSION E40896
KEYWORDS JP 2000166574-A/85.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1 (bases 1 to 729)
Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
Humanized anti-Fas antibody
Patent: JP 2000166574-A 85 20-JUN-2000;
SANKYO CO LTD
OS Homo sapiens (human)
PN JP 2000166574-A/85
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
PR NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO TAMAKI
PC C12N15/09,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
PC C07K16/18,
PC C12N1/21,C12N5/10,C12P21/08/(C12N1/21,C12R1/19),C12N15/00, PC
C12N5/00
CC
FH Key Location/Qualifiers
FT source 1..729
FT /organism="Homo sapiens"
FT /organism="Homo sapiens (human)".
FEATURES
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    Location/Qualifiers
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BASE COUNT 192 a 200 c 182 g 155 t
ORIGIN
Query Match 88.4%; Score 342.2; DB 6; Length 729;
Best Local Similarity 92.8%; Pred. No. 1.2e-101;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy 1 ATGGACATGAGGGTCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 60
Db 7 ATGGACATGAGGGTCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTGGCTCCAGGTGCC 66
Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGACAGA 120
Db 67 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGTCATCTGTAGGGACAGA 126
Qy 121 GTCACATCATTGTCAGGCAAGTCCAGCATATAGGTATATTAAATTGGTATCAGCAG 180
Db 127 GTCACATCATTGTCAGGCAAGTCCAGCATATAGGTATATTAAATTGGTATCAGCAG 186
Qy 181 AAACAGGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTC 240
Db 187 AAACAGGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTCGAAAGTGGGTC 246
Qy 241 CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCCTCAGCAGCCTG 300
Db 247 CCATCAAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTG 306
Qy 301 CAGCTGAAGATTTTGCAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db 307 CAGCTGAAGATTTTGCAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 366
Qy 361 GGCCAGGACCAAGGTGGAATCAA 387
Db 367 GGCCAGGACCAAGGTGGAATCAA 393

RESULT 3
LOCUS MMU57571 Macaca mulatta Ig rearranged light chain variable region, anti-RBC
DEFINITION MMU57571 antibody, mRNA, partial cds.
ACCESSION U57571.1 GI:1575089
VERSION U57571
KEYWORDS
SOURCE Macaca mulatta.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE
1 (bases 1 to 390)
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Db      301 CAACCTGAAGATTTTGCACCTTACTACTGTCAACAGAGTTACAGTACCCCTCAGACGTTTC 360
Qy      361 GCCCAAGGGACCAAGGTGGAATCAAA 387
Db      361 GCCCAAGGGACCAAGGTGGAATCAAA 387

RESULT 5
LOCUS   HUMIGKFN
DEFINITION Human rearranged IgK mRNA VJC region.
ACCESSION M87478
VERSION   1
KEYWORDS C-region; J-region; V-region; immunoglobulin kappa-chain;
          immunoglobulin light chain.
SOURCE   Homo sapiens (individual isolate patient CHEB) bone marrow CDNA to
          mRNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 406)
          Auconturier, P., Bauwens, M., Khamlichi, A.A., Denoroy, L.,
          Spinelli, S., Touchard, G., Preud'homme, J.B. and Cogne, W.
TITLE    Monoclonal Ig L chain and L chain V domain fragment crystallization
          in myeloma-associated Fanconi's syndrome
JOURNAL  J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)
MEDLINE  93224763
PUBMED   8468490
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            /translation="RTVAAP"
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BASE COUNT 97 a 113 c 102 g 94 t
ORIGIN

Query Match      85.9%; Score 332.6; DB 9; Length 406;
Best Local Similarity 91.2%; Pred. No. 1.7e-98;
Matches 353; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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Db      2  ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTCTTGCTCTGGCTCCCGAGTGCC 61
Qy      61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCTCCCTGTCTGTCATCTGTAGGGGACAGA 120
Db      62 AGATGTGACATCCAGATGACCCAGTCTCCATCTCTCCCTGTCTGTCATCTGTAGGGGACAGA 121
Qy      121 GTCACCATCACTTCGAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 180
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Qy      181 AAACAGGAAAGCTCCTTAAGCTCCTGATCTATCTTGTCATCCAGTTTGCAAGTGGGTC 240
Db      182 AAACCGGGAAGCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGTC 241
Qy      241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCATCTCACCCTCAGCAGCCTG 300
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Qy      301 CAGCTTGAAGATTTTGGCACTTATTACTGTCTACAGTTTATAGTACCCTCGGACGTTTC 360
Db      302 CAACTGAAGATTTTGAACCTTACTACTGTCAACAGAGTTACAGTATCCCTGGACGTTTC 361
Qy      361 GGCCAAGGGACCAAGGTGGAATCAAA 387
Db      362 GGCCAAGGGACCAAGGTGGAATCAAA 388

RESULT 6
LOCUS   AF228327
DEFINITION Homo sapiens clone BUS immunoglobulin light chain variable region
          gene, partial cds.
ACCESSION AF228327
VERSION   AF228327.1
KEYWORDS GI:9295292
SOURCE   Homo sapiens.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 400)
          Maloum, K., Dighiero, G. and Magnac, C.C.
          Unmutated Ig VH genes in CLL patients
          Unpublished
          2 (bases 1 to 400)
          Maloum, K., Dighiero, G. and Magnac, C.C.
          Direct Submission
          Submitted (13-JAN-2000) Physiopathology, Institut Pasteur, 28 rue
          du Dr Roux, Paris 75015, France
          Location/Qualifiers
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BASE COUNT 99 a 109 c 100 g 92 t
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[illegible]

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ALIGNMENT

RESULT 1
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LOCUS
DEFINITION
IMAGE:3057290.5, mRNA sequence.
ACCESSION
AW405753
VERSION
AW405753.1
KEYWORDS
EST
SOURCE
human
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 493)
NIH-MGC http://mgs.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Genome Project
JOURNAL
Unpublished (1999)
COMMENT
Email: cga@nci.nih.gov
ECO RI site shown at the beginning of the sequence
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Prepared by: M.B. Soares Ltd
CDNA Sequencing by: M.B. Soares Ltd
Clone distribution: MGC clone distribution
found through the I.M.A.G.E. Consortium
www.bio.illnl.gov/bbtp/imaoc/imaoc.html
Seq primer: M13 Forward
Location/Qualifiers
1..493

SNOWFLAKE

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3	BQ540787	423	14	BQ540787	602570674	
4	BQ67106	423	14	BQ67106	AGENCOURT	
5	BQ537031	423	14	BQ537031	602565115	
6	BQ754732	423	14	BQ754732	602714301	

Read No. is the number of results predicted by chance to have a score higher than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 /note="Vector: pRTT3-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

117 a 138 c 119 g 119 t

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Qy 63 ATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGAGT 122
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Qy 123 CACCATCACTTCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAA 182
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Qy 183 ACCAGGAAAGTCTTAAGTCTCTGATCTATGTTGATCCAGTTTGCAGAGTGGGTC 242
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Qy 243 ATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCAGCGTCAGCAGCGTCA 302
 Db 248 ATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCAGCATCAGCAGTCTGA 307

Qy 303 GCCTGAAGATTTGGCAGTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTCCG 362
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Qy 363 CCAAGGACCAAGTGGAAATCAA 387
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 LOCUS AGENCOURT_8616470 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302159
 DEFINITION 5', mRNA sequence.

ACCESSION BQ882857
 VERSION BQ882857
 KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 923)

TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LICM2519 row: c column: 24
 High quality sequence stop: 672.

FEATURES
 source

Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6302159"

/clone_lib="NIH_MGC_113"

/lab_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGCAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH MGC Library."

219 a 274 c 224 g 201 t 5 others

BASE COUNT

ORIGIN

Query Match 88.0%; Score 340.6; DB 14; Length 923;

Best Local Similarity 92.5%; Pred. No. 2.1e-95;

Matches 358; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTGTCTCTGGTCCCGAGTGC 60
 Db 13 ATGACATGAGGGTCCCGCTCAGCTCTGGGGTCTCTGTCTCTGGTCCCGAGTGC 72

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 120
 Db 73 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGA 132

Qy 121 GTACCATCACTTCAGGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
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Qy 181 AAACCCAGGAAAGTCTTAAGTCTCTGATCTATCTTGCATCCAGTTTGCAGAGTGGGTC 240
 Db 193 AAACCCAGGAAAGTCTTAAGTCTCTGATCTATCTTGCATCCAGTTTGCAGAGTGGGTC 252

Qy 241 CCATCAAGGTTTCAGCGGCAAGTCTGGGACAGAGTTCACCTCTCAGCGTCAGCAGCTG 300
 Db 253 CCATCAAGGTTTCAGCGGCAAGTCTGGGACAGAGTTCACCTCTCAGCATCAGCAGCTG 312

Qy 301 CAGCTGAAGATTTTGGGACATTATCTGTCTACAGTTTATAGTACCCCTCGGACGCTC 360
 Db 313 CAACCTGAAGATTTTGGGACATTATCTGTCTCAACAGACTTACATTTACCCCTCGGACGCTC 372

Qy 361 GGCCAAAGGCAAGTGGAAATCAA 387
 Db 373 GGCCAAAGGCAAGTGGAAATCAA 399

RESULT 3
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 LOCUS BQ540787

DEFINITION 602570674F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695114 5',

mRNA sequence.

ACCESSION BQ540787

VERSION BQ540787.1 GI:13533020

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 891)

TITLE NIH-MGC http://mgi.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.


```

KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 724)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1506 row: m column: 04
High quality sequence stop: 573.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4689963"
/clone_lib="NIH MGC 77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggccattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
BASE COUNT 190 a 204 c 181 g 145 t
ORIGIN
Query Match 85.2%; Score 329.6; DB 12; Length 724;
Best Local Similarity 92.3%; Pred. No. 5e-92;
Matches 358; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
QY 1 ATGGACATGAGGTCCCGCTCAGCTCCCTGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db |||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGA 120
Db |||||
QY 85 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGA 144
Db |||||
QY 121 GTCACATCATTGACGGCAAGTCAGGACATTAGGTATTTAAATTTGGTATCAGCAG 180
Db |||||
QY 145 GTCACCATCACTTGGCGGCAAGTCAGGACATTAGGAGCTATTTAAATTTGGTATCAGCAG 204
Db |||||
QY 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTGATCCAGTTTGCAGATGGGGTC 240
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QY 205 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTGATCCAGTTTGCAGATGGGGTC 264
Db |||||
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QY 325 GCAACCTGAAGATTTTGCAGCTTACTACTGTCAACAGAGTTTACAGTAACCCCTCGACGTT 384
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QY 360 CGGCCAAGGACCAAGGTGGAATCAAA 387
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QY 385 CGGCCAAGGACCAAGGTGGCAATCAAA 412
Db |||||

RESULT 6
BG754732
LOCUS 602714301P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854409 5',
DEFINITION mRNA sequence.
ACCESSION BG754732
VERSION BG754732.1 GI:14065385
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Prepared by: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1702 row: a column: 02
High quality sequence stop: 805.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Size-selected
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 225 a 245 c 215 g 182 t
ORIGIN
Query Match 85.1%; Score 329.4; DB 12; Length 867;
Best Local Similarity 90.7%; Pred. No. 6.5e-92;
Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGTCCCGCTCAGCTCCCTGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db |||||
QY 19 ATGGACATGAGGTCCCGCTCAGCTCCCTGGGCTTCTGCTCTGGCTCCAGGTGCC 78
Db |||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGA 120
Db |||||
QY 79 AGATGTGACATCCAGTGTGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGACAGA 138
Db |||||
QY 121 GTCACCATCACTTCAGGGGCAAGTCAGGACATTAGGTATTTAAATTTGGTATCAGCAG 180
Db |||||
QY 139 GTCACCATCACTTCAGGGGCAAGTCAGGACATTAGGAGTCTTTAGCCCTGGTATCAGCAG 198
Db |||||
QY 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTGATCCAGTTTGCAGATGGGGTC 240
Db |||||
QY 199 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTGATCCAGTTTGCAGATGGGGTC 258
Db |||||
QY 241 CCATCAAGTTCAGCGGAGTGGATCTGGGACAGAGTTTCACTCACCCTCAGCAGCCTG 300
Db |||||
QY 259 CTTCAAGTTTCAGGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 318
Db |||||
QY 301 CAGCCTGAAGATTTTGGACATTATTACTGTCTAAGGTTTATAGTACCCCTCGGACGTT 360
Db |||||

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QY 121 GTCACCATCACTTGCCAGGCAAGTCAGGACATTAGGTATTTATTTAAATTTGGTATCAGCAG 180
 |||||
 Db 147 GTCACCATCACTTTCGCGGCAAGTCACAGCATTAGCAACTATTTAAATTTGGTATCAGCAG 206
 |||||
 QY 181 AAACCAAGAAAGCTCTTAAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGTC 240
 |||||
 Db 207 AAACCAAGAAAGCTCTTAAGCTTCCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGTC 266
 |||||
 QY 241 CCATCAAGGTTTCAGCGGCAAGTCAGTCTGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
 |||||
 Db 267 CCATCAAGGTTTCAGTGGCAGTGGATCTGGACAGATTTCACTCTCACCATCAGCATCTG 326
 |||||
 QY 301 CAGCCTGAAGATTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTC 360
 |||||
 Db 327 CAACTTGAAGATTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTC 386
 |||||
 QY 361 GCGCAAGGACCAAGGTGGAATCAAA 387
 |||||
 Db 387 GCGCAAGGACCAAGGTGGAATCAAA 413

RESULT 9
 AW404992 391 bp mRNA linear EST 16-FEB-2000
 LOCUS
 DEFINITION
 UI-HF-BL0-abx-a-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3058060 5', mRNA sequence.

ACCESSION
 AW404992
 VERSION
 AW404992.1 GI:6924049

KEYWORDS
 EST.

SOURCE
 human.

ORGANISM
 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 391)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.biol.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

FEATURES

source

1. .391

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3058060"

/clone_lib="NIH_MGC_37"

/tissue_type="lymph"

/cell_line="germinal center B cells"

/lab_host="MGC85"

/lab_host="DH10B (LT1)"

/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

98 a 108 c 94 g 91 t

BASE COUNT

ORIGIN

Query Match 84.4%; Score 326.6; DB 10; Length 391;

Best Local Similarity 91.1%; Pred. No. 2.9e-91;

Matches 347; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCAGTCTCGGGCTCTCTCTCTGCTCCAGGTCAGATGT 66

|||||

Db 5 AGGAGGTCCTCCAGTCTCGGGCTCTCTCTCTGCTCCAGGTCAGATGT 64

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGAGTCACC 126
 |||||
 Db 65 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGAGTCACC 124
 |||||
 QY 127 ATCACTTCGAGGGCAAGTCAGACATTAGGTATTTATTTAAATTTGGTATCAGAGAAACA 186
 |||||
 Db 125 ATCACTTCCCGGCAAGTCAGAGCATTAGCAGCTATTTAAATTTGGTATCAGAGAAATCA 184
 |||||
 QY 187 GGAAAGCTCCTTAGCTCCTGATCTATGTTGCACTCCAGTTTGCAGAGTGGGTCCTCATCA 246
 |||||
 Db 185 GGGAAAGCCCTTAGCTCCTGATCTATGTTGCAAGTGGGTCCTCATCA 244
 |||||
 QY 247 AGGTTACAGGGCAGTGGGATCTGGGACAGAGTTCACTCTCACCGTCAGAGCCTCGAGCCT 306
 |||||
 Db 245 AGGTTACAGGGCAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGAGTCTCAACCT 304
 |||||
 QY 307 GAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCGTTTCGGCCAA 366
 |||||
 Db 305 GAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCGTTTCGGCCAA 364
 |||||
 QY 367 GGGACCAAGTGGGAATCAAA 387
 |||||
 Db 365 GGGACCAAGTGGGAATCAAA 385
 |||||

RESULT 10

AW383563

LOCUS

DEFINITION

PM4-HT0348-261199-001-A07 HT0348 Homo sapiens cDNA, mRNA sequence.

ACCESSION

AW383563

VERSION

AW383563.1 GI:6888131

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel.: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM4&t2=PM4-HT0348-

261199-001-A07&t3=1999-11-26&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 452.

Location/Qualifiers

1. 453

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0348"

/dev_stages="Adult"

/note="Organ: head neck; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

108 a 125 c 107 g 113 t

BASE COUNT

ORIGIN

Query Match 84.3%; Score 326.2; DB 10; Length 453;

Best Local Similarity 90.2%; Pred. No. 4.2e-91;

ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 248 a 235 g 220 t
ORIGIN

Query Match 84.3%; Score 326.2; DB 14; Length 992;
Best Local Similarity 90.2%; Pred. No. 7.1e-91;
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCTCGGGCTCTTCTGCTCTGGCTCCACGGTCC 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 32 ATGGACATGAGGTCCTCCGCTCAGCTCTCGGGCTCTTCTGCTCTGGCTCCACGGTCC 91
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 92 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 151
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 GTCACATCACTTGGCAGGCAAGTCAGGACATAGGATATTTAAATTGGTATCAGCAG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 152 GTCACATCACTTGGCAGGCAAGTCAGGACATAGGATATTTAAATTGGTATCAGCAG 211
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 AAACAGGAAAGCTCCCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAGTGGGCTC 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 212 AAACAGGAAAGCTCCCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAGTGGGCTC 271
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CCATCAAGGTTTCCAGGCGAGTGGATCTGGGACAGAGTTCACCTCTCAGCGTCAGACGCTG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 272 CCATCAAGGTTTCCAGGCGAGTGGATCTGGGACAGAGTTCACCTCTCAGCGTCAGACGCTG 331
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 CAGCTGAAGATTTTCCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 332 CAACCTGAAGATTTTGCACCTTACTGTCAACAGAGTTACATTTACCCCTGGACGTTTC 391
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GCCCAAGGACCAAGGTGGAAATCAA 387
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 392 GCCCAAGGACCAAGGTGGAAATCAA 418
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 13
LOCUS B0706786 964 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7976126 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214887
5', mRNA sequence.

ACCESSION B0706786
VERSION B0706786
KEYWORDS EST.

SOURCE B0706786.1 GI:21845685

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 964)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCW2382 row: 0 column: 16

High quality sequence stop: 659.

Location/Qualifiers

1..964

/organism="Homo sapiens"

FEATURES
source

/db xref="taxon:9606"
/clone="IMAGE:6214887"
/clone_lib="NIH_MGC_113"

/lab_host="DH10B (phage-resistant)"

/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."

BASE COUNT 239 a 280 c 230 g 212 t 3 others
ORIGIN

Query Match 84.0%; Score 325.2; DB 14; Length 964;
Best Local Similarity 90.2%; Pred. No. 1.4e-90;
Matches 348; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY 1 ATGCACATGAGGTCCTCCGCTCAGCTCTCGGGCTCTTCTGCTCTGGCTCCACGGTCC 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 15 ATGCACATGAGGTCCTCCGCTCAGCTCTCGGGCTCTTCTGCTCTGGCTCCACGGTCC 74
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 75 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 134
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 GTCACATCACTTCCAGGCGAAGTCAGGACATAGGATATTTAAATTGGTATCAGCAG 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 135 ATCACCATCACTTCCGCGGCAAGTCAGAACATTTTAAATTGGTATCAGCAG 194
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 AAACAGGAAAGCTCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAGTGGGCTC 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 195 AAACAGGAGAGCCCTAATCTCTGATCTTACTGCACTCCAGTTTGCAGTGGGCTC 254
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 CCATCAAGGTTTCCAGGCGAGTGGATCTGGGACAGAGTTCACCTCTCAGCGTCAGACGCTG 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 255 CCATCAAGGTTTCCAGGCGAGTGGATCTGGGACAGAGTTCACCTCTCAGCGTCAGACGCTG 314
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 CAGCTGAAGATTTTCCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTC 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 315 CAACCTGAAGATTTTGCACCTTACTGTCAACAGAGTTACATTTACCCCTGGACGTTTC 374
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 GCCCAAGGACCAAGGTGGAAATCAA 386
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 375 GCCCAAGGACCAAGGTGGAAATCAA 400
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 14
LOCUS AW405752

DEFINITION UI-HF-BLO-abb-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone

IMAGE:13057288 5', mRNA sequence.

ACCESSION AW405752

VERSION AW405752.1 GI:6924809

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 447)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:


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FT      /note= "encodes CDR 2 region"
FT      331..357
FT      /*tag= f
FT      /note= "encodes CDR 3 region"
FT
XX
PN      WO9837099-A1.
XX
PD      27-AUG-1998.
XX
XX      17-FEB-1998; 98WO-US02253.
XX
XX      05-FEB-1998; 98US-0803085.
XX      20-FEB-1997; 97US-0803085.
XX      (IDEC-) IDEC PHARM CORP.
XX      (SEK) SEIKAGAKU CORP.
XX
PI      Klotzer WS, Nakamura T, Reff ME;
XX
XX      WPI; 1998-467495/40.
XX      P-PSDB; AAW70379.
XX
XX      New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX      expression to treat or prevent allergic, inflammatory and
XX      auto:immune conditions
XX
XX      Example 1; Pages 106-108; 146pp; English.
XX
XX      The present sequence represents a DNA sequence encoding the light
XX      chain variable region of primate monoclonal antibody anti-human CD23 588.
XX      The invention provides primate monoclonal antibodies which specifically
XX      bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX      and comprise either of a human gamma-1 or human gamma-3 constant region
XX      that binds to human Fc gamma receptors and inhibits IgE expression.
XX      The monoclonal antibodies of the invention are claimed to be useful
XX      for inhibiting induced IgE production for treating or preventing
XX      allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX      conjunctivitis, autoimmune haemolytic anaemia, etc.
XX
XX      Sequence 387 BP; 92 A; 102 C; 98 G; 95 T; 0 other;
XX
XX      Query Match      100.0%; Score 387; DB 19; Length 387;
XX      Best Local Similarity 100.0%; Pred. No. 1.le-108;
XX      Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1  ATGGACATCAGGTCCTCCGCTCAGCTCCTGGGCTCTTCTGCTCCAGGTGCC 60
Db      |||
QY      1  ATGGACATCAGGTCCTCCGCTCAGCTCCTGGGCTCTTCTGCTCCAGGTGCC 60
Db      |||
QY      61  AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
Db      |||
QY      61  AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
Db      |||
QY      121  GTCACCATCCTTGCAGGCGAAGTCAGGACATTAGGTATTATTAATTGGTATCAGCAG 180
Db      |||
QY      121  GTCACCATCCTTGCAGGCGAAGTCAGGACATTAGGTATTATTAATTGGTATCAGCAG 180
Db      |||
QY      181  AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTCATCCAGTTGCAAGTGGGTC 240
Db      |||
QY      181  AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTCATCCAGTTGCAAGTGGGTC 240
Db      |||
QY      241  CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGACGCTG 300
Db      |||
QY      241  CCATCAAGGTTTCAGCGGCAAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGACGCTG 300
Db      |||
QY      301  CAGCCTGAAGATTTTCGCACTTATTACTCTTACAGGTTTATAGTACCCCTCGGACGTT 360
Db      |||
QY      301  CAGCCTGAAGATTTTCGCACTTATTACTCTTACAGGTTTATAGTACCCCTCGGACGTT 360
Db      |||
QY      361  GCCCAAGGACCAAGGTGAAATCAA 387
Db      |||
QY      361  GCCCAAGGACCAAGGTGAAATCAA 387
Db      |||
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```
RESULT 2
AAV61794
ID      AAV61794 standard; DNA; 19035 BP.
XX
AC      AAV61794;
XX
DT      07-JUN-1999 (first entry)
XX
DE      Traget plasmid Mandy containing anti-CD23 gene.
XX
KW      Mandy; target plasmid; gene integration; gene amplification;
KW      homologous recombination; vector; neomycin phosphotransferase;
KW      neo gene; selectable marker; immunoglobulin; CD23; 588; human; ss.
XX
OS      Chimeric - Mus sp.
OS      Chimeric - Escherichia coli.
OS      Chimeric - Baculovirus.
OS      Chimeric - Cytomegalovirus.
OS      Chimeric - Rhesus macaque polyoma virus.
OS      Chimeric - Photinus sp.
OS      Chimeric - Salmonella typhimurium.
OS      Chimeric - Homo sapiens.
XX
FH      Key
FH      Location/Qualifiers
FT      misc_feature
FT      361
FT      /*tag= a
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT
FT      misc_feature
FT      721
FT      /*tag= b
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
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FT      misc_feature
FT      2941
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FT      /note= "this base represents a nucleotide missing
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FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
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FT      misc_feature
FT      3301
FT      /*tag= d
FT      /note= "this base represents a nucleotide missing
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FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT
FT      misc_feature
FT      4261
FT      /*tag= e
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT
FT      misc_feature
FT      4621..4622
FT      /*tag= f
FT      /note= "these bases represent nucleotides missing
FT      from the sequence given in the
FT      specification. They are included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT
FT      misc_feature
FT      8161
FT      /*tag= g
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT
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181	AAACCAAGGAAAGCTCTTAAGCTCTGATCTATATGTCATCCAGTTTGCAAGTGGGGTC	240
259	AAACCAAGGAAAGCCCTTAAGCTCTGATCTATGTCATCCANTTTGCAAGTGGGGTC	318
241	CCATCAAGGTTTCAGCGGCAGTGGATCTGGGACACAGTTCACTCAACGTCAGCAGCTG	300
319	CCATCAAGGTTTCAGTGGGAGTGGATCTGGGACAGATTCACTATCAACCATCAGCAGCTG	378
301	CAGCCTGAAGATTTTGGCACTTATTACTGTCCTACAGGTTTATAGTACCCCTCGAGCGTTC	360
379	CARCTGAAGATTTTGGCACTTATCTGTCTCAACAGTATGATATATGATATGATTCCTCTC	438
361	GGCCAAAGGACCAAGGTGGAAATCAAA	387
439	GGCRRAGGAGACCAAGGTGGATCAAA	465

RESULT 6
AAT75423
ID AAT75423 standard; cDNA; 396 BP.

DT 12-SEP-1997 (first entry)

XX	Human anti-tumour antigen antibody light chain variable region cDNA.
DE	

Human; tumour antigen; cancer; monoclonal; antibody; light chain; variable region; medicine; pharmacology; biochemistry; ds.

OS Homo sapiens.

AA	Key	Location/Qualifiers
FH		
FT	sig peptide	1..66

JP09100300-A.

XX PD 15-APR-1997.

XX 03-OCT-1995: 95JP-0278266.

XX
PR 03-OCT-1995: 95JP-0278266-XX
PA (HAGT /) HAGIWARA Y.XX
WPT: 1997-276726/25

DR P-PSDB; AAW22842.
YY

Anticancer human monoclonal antibody variable region sequences - and related DNA and RNA

PS Claim 12; Page 11; 14pp; Japanese.

The present sequence encodes a human anti-tumour antigen monoclonal antibody (MAB) light chain variable region, useful in medicine, pharmacology and biochemistry. The isotype of a MAB secreted by the human/human hybridoma HT was determined to be μ and kappa. Human MAB was purified, and the antigen recognised by human MAB CLN'-IgM identified by western blotting.

Sequence 396 BP; 101 A; 107 C; 97 G; 91 T; 0 other;

	Query Match	86.4%	Score 334.2	DB 18	Length 396
	Best Local Similarity	91.5%	Pred. No. 1.8e-92		
	Matches 354	Conservative	0	Mismatches 33	Indels 0
Qy	1	ATGGACATGAGGTTCCCGCTCAGCTCCTCGGGGCTCTTGTCTCGCTCCAGGTGCC	60		
		1			
Db	1	ATGGACATGAGGCCACGTTCACTCTCGGGCTCTGTACTCTGGCTCCAGGTGCC	60		

DT 03-OCT-2000 (first entry)
XX DNA encoding the kappa chain of immunoglobulin clone 11.2.1.1.
DE
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 67..714
FT /*tag= a
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US30895.
XX
XX 23-DEC-1998; 98US-0113647.
XX (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG,
PI Corvalan JR;
PI
XX WPI; 2000-442647/38.
DR P-PSDB; AAY93735.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen
PT (CTLA)-4 containing specified heavy and light chain sequences, useful
PT for treating, e.g. immune disorders
XX
XX Example 2; Fig 22r; 157pp; English.
XX
XX The present sequence encodes a kappa chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen
CC (CTLA)-4. Antibodies of the invention are composed of a heavy chain
CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.
XX
SQ Sequence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;
Query Match 84.3%; Score 326.2; DB 21; Length 714;
Best Local Similarity 90.2%; Pred. No. 6.3e-90;
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTTCTCTGCTCGCTCCAGGTGCC 60
DB 1 ATGGACATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTTCTCTGCTCGCTCCAGGTGCC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGGGACAGA 120
DB 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGGGACAGA 120
QY 121 GTCCACATCAGTTGGAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
DB 121 GTCCACATCAGTTGGAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
QY 181 AAACACGAGAAAGCTCTTAAGCTCTCTGATCTATGTTGTCATCCAGTTTGCAAGTGGGTC 240
DB 181 AAACACGAGAAAGCTCTTAAGCTCTCTGATCTATGTTGTCATCCAGTTTGCAAGTGGGTC 240
QY 241 TCATCAAGGTTGAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCCTGACGACCTG 300

DB 241 CCATCAAGGTTCACTGGCAGTGGATCTGGGACAGATTCTCACTCTCACCATCAGCAGTGTG 300
QY 301 CAGCTCAAGATTTTTCGACTTATTACTGTCTACAGGTTTATAGTACCTCGGACGTTTC 360
DB 301 CAACCTGAAGATTTTTCGACTTATTACTGTCTACAGGTTTATAGTACCTCGGACGTTTC 360
QY 361 GGCCCAAGGGACCAAGTGGAAATCAAA 387
DB 361 GGCCCTGGGACCAAGTGGAAATCAAA 387
RESULT 10
AAZ39327
ID AAZ39327 standard; DNA; 387 BP.
XX
XX AAZ39327;
AC
XX 15-FEB-2000 (first entry)
DT
DE Nucleotide sequence of chimpanzee V kappa cDNA clone 46-14.
XX
XX Complementarity determining region; antibody; primate; immunogenicity;
KW Old World ape; Old World monkey; antigen-binding affinity; ss.
XX
XX Pan troglodytes.
OS
XX WO9955369-A1.
PN
XX 04-NOV-1999.
PD
XX 28-APR-1999; 99WO-US09131.
PF
XX 28-APR-1998; 98US-0083367.
PR
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA
XX Taylor AH;
PI
XX WPI; 2000-023265/02.
DR P-PSDB; AAY56659, AAY56724.
XX
XX Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
XX Example 2; Page 67-68; 123pp; English.
XX
XX The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
SQ Sequence 387 BP; 94 A; 104 C; 95 G; 94 T; 0 other;
Query Match 83.9%; Score 324.6; DB 21; Length 387;
Best Local Similarity 89.9%; Pred. No. 1.1e-89;
Matches 348; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTTCTGCTCTCGCTCCAGGTGCC 60
DB 1 ATGGACATGAGGGTCCCCGCTCAGCTCTCTGGGGCTCTTCTGCTCTCGCTCTCAGGTACC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGAGGGACAGA 120
DB 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGAGGACAGA 120
QY 121 GTCCACATCAGTTGGAGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180

CC of multiple isotypes by undergoing isotype switching. These animals
CC produce a first Ig type that is necessary for antigen-stimulated B-cell
CC maturation and can switch to encode and produce one or more subsequent
CC heterologous isotypes.

XX SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
PS Query Match 82.2%; Score 318.2; DB 18; Length 388;
XX Best Local Similarity 88.9%; Pred. No. 1.4e-87;
CC Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGGACATGATGTTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGTTCAGGTTC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTAGGGACAGA 120
Db 61 AGATGCGACATCCAGATGACCCAGTCTCCATCTCCGTGTCTGCACTGTAGGACAGA 120

Qy 121 GTCCACATCACTTTCAGGGCAAGTCAGGACATTAGTATTATTTAAATTGGTATCAGCAG 180
Db 121 GTCCACATCACTTTCAGGGCAAGTCAGGACATTAGTATTATTTAAATTGGTATCAGCAG 180

Qy 181 AAACACGAGAAAGCTCTTAAGCTCTCTGATCTATGTTGATCCAGTTTGCAAAGTGGGTC 240
Db 181 AAACACGAGAAAGCTCTTAAGCTCTCTGATCTATGTTGATCCAGTTTGCAAAGTGGGTC 240

Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCACCGTCAGACGCTG 300
Db 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCACCGTCAGACGCTG 300

Qy 301 CAGCCTGAAGATTTTCGCACTTATTACTCTCTACAGGTTTATAGTACCCCTCGGACGTT 360
Db 301 CAGCCTGAAGATTTTCGCACTTATTACTCTCTACAGGTTTATAGTACCCCTCGGACGTT 360

Qy 361 GCCCAGGGACCAAGGTGGAAATCAAA 387
Db 361 GCCCAGGGACCAAGGTGGAGATCAAA 387

RESULT 13
AAV39239
ID AAV39239 standard; DNA; 388 BP.
XX AC AAV39239;
XX DT 18-DEC-1998 (first entry)

DE Functional Kappa transcript isolated from transgenic cell line 10C5.
KW Transgenic animal; human heterologous antibody; transgene;
KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW autoimmune reaction; inflammatory response; transplant rejection;
KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; ss.

OS Synthetic.
OS Homo sapiens.
OS Mus sp.

XX W09824884-A1.
XX 11-JUN-1998.
XX 01-DEC-1997; 97WO-US21803.
XX 02-DEC-1996; 96US-0758417.
XX (GENP-) GENPHARM INT.
XX Kay RM, Lönberg N;
XX

DR WPI; 1998-333306/29.
XX Hybridoma producing antibody specific for interleukin-8 - used to
PT prevent efflux of neutrophils from vasculature, and treat
PT reperfusion injury
XX Example 41; Page 304; 452pp; English.

PS AAV39232-41 represent functional transcripts of a human IGGKappa
XX anti-CD4 antibody. The sequences are isolated from 5 different
CC transgenic mouse hybridoma cell lines. The specification describes
CC transgenic non-human animals, especially a mouse, which are capable of
CC producing a human heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. The transgenic animals have human heavy and
CC light chain transgenes. The transgenes are capable of functionally
CC rearranging a heterologous diversity (D) gene in a
CC variable-diversity-junction (V-D-J) recombination. The transgenes include
CC a heavy chain transgene comprising at least one V, D and J gene segment,
CC and one constant region gene segment. The immunoglobulin (Ig) light chain
CC transgene comprises at least one V and J gene segment and one constant
CC region gene segment. The gene segments are heterologous to the transgenic
CC animal. The antibody can be used to prevent efflux of neutrophils from
CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC antibodies are used to reduce undesirable autoimmune reactions. The
CC inflammatory responses and rejection of transplanted organs. The
CC anti-IL-8 antibodies can reduce tissue damage and prolong survival in
CC animal models of acute adult respiratory distress syndrome (ARDS) and
CC acid induced lung injury. The anti-IL-8 antibodies can also be used for
CC the treatment of vasculitis, septic shock, allergic reactions (e.g.
CC asthma) and cystic fibrosis.

XX SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
PS Query Match 82.2%; Score 318.2; DB 19; Length 388;
XX Best Local Similarity 88.9%; Pred. No. 1.4e-87;
CC Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 1 ATGGACATGAGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGGACATGATGTTCCCGCTCAGCTCTGGGGCTCTTCTGCTCTGGTTCAGGTTC 60

Qy 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCACTGTAGGGACAGA 120
Db 61 AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCACTGTAGGACAGA 120

Qy 121 GTCCACATCACTTTCAGGGCAAGTCAGGACATTAGTATTATTTAAATTGGTATCAGCAG 180
Db 121 GTCCACATCACTTTCAGGGCAAGTCAGGACATTAGTATTATTTAAATTGGTATCAGCAG 180

Qy 181 AAACACGAGAAAGCTCTTAAGCTCTCTGATCTATGTTGATCCAGTTTGCAAAGTGGGTC 240
Db 181 AAACACGAGAAAGCTCTTAAGCTCTCTGATCTATGTTGATCCAGTTTGCAAAGTGGGTC 240

Qy 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCACCGTCAGACGCTG 300
Db 241 CCATCAAGTTTCAGGGCAGTGGATCTGGGACAGATTCACTCTCACCGTCAGACGCTG 300

Qy 301 CAGCCTGAAGATTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTT 360
Db 301 CAGCCTGAAGATTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTT 360

Qy 361 GCCCAGGGACCAAGGTGGAAATCAAA 387
Db 361 GCCCAGGGACCAAGGTGGAGATCAAA 387

RESULT 14
AAZ21993
ID AAZ21993 standard; DNA; 388 BP.
XX AC AAZ21993;
XX DT 24-NOV-1999 (first entry)

SQ Sequence 936 BP; 239 A; 276 C; 214 G; 207 T; 0 other;

Query Match 82.2%; Score 318; DB 21; Length 936;
Best Local Similarity 90.3%; Pred. No. 2.3e-87;
Matches 352; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGGTGCC 60
Db |||||
QY 19 ATGGACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCAGGTGCC 78
Db |||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTCTGCTATCTGTAGGGACAGA 120
Db |||||
QY 79 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTCTGCTATCTGTAGGACAGA 138
Db |||||
QY 121 GTCACCATCACCTTGCAGGGCAAGTCAGGACATTAGGTATTATTAAATTGGTATCAGCAG 180
Db |||||
QY 139 GTCACCATCACCTTGCAGGGCAAGTCAGGACATTAGGCTATTAAATTGGTATCAGCAG 198
Db |||||
QY 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGTC 240
Db |||||
QY 199 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGCTGCTCAGTTTGCAAGTGGGTC 258
Db |||||
QY 241 CCATCAGGTTTCCAGGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTACAGCCTG 300
Db |||||
QY 259 CCATCAAGGTTTCCAGGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTG 318
Db |||||
QY 301 CAGCCTGAAGATTTTCCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGG--ACG 357
Db |||||
QY 319 CAACCTGAAGATTTTGCAACTTACTGTCAACAGAGTTACAGTACCCCTCCGATCACC 378
Db |||||
QY 358 TTCGGCCAAAGGACCAAGGTGGAAATCAA 387
Db |||||
QY 379 TTCGGCCAAAGGACACAGACTGGAGATTAA 408
Db |||||

Search completed: July 15, 2003, 08:27:58
Job time : 148.296 secs

Corporate Services Ltd.
11111 Corporate Blvd.

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CXX g++ -std=c++11 -c cell.cc, using SW method
Run : ./cell_test_04_08_09 /dev/null 100.173 Seconds
      without alignments!
      620.147 Million cell updates/sec

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[illegible][illegible]

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[illegible]

• 100% Satisfaction Guarantee

3. *0-mz 6/p/odata/1/purpna/US64 PURCOMB.seq: **
4. *0-mz 6/p/odata/1/purpna/US64 PURCOMB.seq: **
5. *0-mz 6/p/odata/1/purpna/POTUS PURCOMB.seq: **

b: /pnp/ 5/pdata/1/pnpna/usca NEW_PUB.seq: *
 c: /pnp/ 5/pdata/1/pnpna/usca PUBCOMB.seq: *
 d: /pnp/ 5/pdata/1/pnpna/usca PUBCMB.seq: *
 e: /pnp/ 5/pdata/1/pnpna/usca PUBCMB.seq: *

[illegible]

14. `compdata: a1/pulpina/US99_PUBCOMPR.seq *`

and is derived by analysis of the total score distribution.

Result	Every year	At least once in 10 years	Description
None			

Sequence	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Sequence 1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Sequence 2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Sequence 3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Sequence 4	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Sequence 5	1	2	3	4																																																																																																

4	6.09	7.47	10.3	4.93	38	Sequence 27
4	6.09	7.47	10.3	4.93	39	Sequence 28
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;	TOPOLOGY: linear	
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;	FEATURE:	
;	NAME/KEY: CDS	
;	LOCATION: 1..387	
;	FEATURE:	
;	NAME/KEY: mat_peptide	
;	LOCATION: 67..387	
;	SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
;	US-10-103-686-3	
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	Best Local Similarity	100.0%; Pred. No. 2.4e-114;
	Matches 387; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Qy	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Qy	121	GTCACCATCACTTGAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
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Qy	181	AAACGAGGAAAAGTCTCTAAGCTCTGTATCTATGTTGCATCCAGTTTGCAAAGTGGGTC 240
Db	181	AAACGAGGAAAAGTCTCTAAGCTCTGTATCTATGTTGCATCCAGTTTGCAAAGTGGGTC 240
Qy	241	CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCATCTCACCGTCAGCAGCGTC 300
Db	241	CCATCAAGGTTTCAGGGCAGTGGATCTGGGACAGAGTTTCATCTCACCGTCAGCAGCGTC 300
Qy	301	CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCTTCGGACGTTTC 360
Db	301	CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCTTCGGACGTTTC 360
Qy	361	GGCCAAGGGACCAAGGTGGAATCAAA 387
Db	361	GGCCAAGGGACCAAGGTGGAATCAAA 387

RESULT 2
US-09-019-441-3
Sequence 3, Application US/09019441
Publication No. US20030086921A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: 35
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
City: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/803,085

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; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..387
;
; NAME/KEY: mat_peptide
; LOCATION: 67..387
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-019-441-3
Query Match 100.0%; Score 387; DB 9; Length 387;
Best Local Similarity 100.0%; Pred No. 2.4e-114;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGTGCCCGCTCAGCTCCTGGGCTCCTTCTGTCTCGCTCCAGGTGCC 60
DB 1 ATGGACATGAGGTGCCCGCTCAGCTCCTGGGCTCCTTCTGTCTCGCTCCAGGTGCC 60
QY 61 AGATGTGACATCAGATGACCCAGTCCCATCTTCCTGTCTGCATCTGTAGGGGACAGA 120
DB 61 AGATGTGACATCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTGTAGGGGACAGA 120
QY 121 GTCACCATCACTTTCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
DB 121 GTCACCATCACTTTCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
QY 181 AACCAGGAAAGCTCTAGCTCCTGATCTATGTTCATCCAGTTTGCAAAGTGGGTC 240
DB 181 AACCAGGAAAGCTCTAGCTCCTGATCTATGTTCATCCAGTTTGCAAAGTGGGTC 240
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QY 301 CAGCTGAAGATTTTGGCACTTATTAATCTGTCTACAGTTTATAGTACCCCTCGGACGTTTC 360
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RESULT 3
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; Sequence 125, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09

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; Sequence 186, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 529
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-186

Query Match 83.0%; Score 321.4; DB 9; Length 537;
Best Local Similarity 89.4%; Pred. No. 3.2e-93;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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Db 503 ATGGACATGAGGTCCCGCTCAGCTCTGGGGCTCCTCTGCTTGGCTCCAGATACC 444
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Db 443 AGATGTGACATCCAGATGACCAGTCTCCATCTTCCCTGTGTCATCTGTAGGACAGA 384
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Db 203 CAGCCTGAAGATTTTTCGAACTTATTTCTGCAAAAATAATACAGTGGCCCGGAGCCTTC 144
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RESULT 12
US-10-040-244-13
; Sequence 13, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 13
; LENGTH: 716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-13

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Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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Qy 121 GTCACCATCCTTGCAGGCAAGTCAGGACATTAGGTATTTAAATTTGGTATCAGCAG 180
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Qy 181 AAACAGGAAAGCTCCTTAAGCTCTGATCTATGTGATCCAGTTTGCAGAGTGGGTC 240
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Db 287 CCATCAAGGTTTCAGCGGAGTGGATTTGGGACAGATTTCACTCTCACCATCGGAGCCTG 346
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RESULT 13
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; Sequence 13, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:


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Qy 301 CAGCCTGAGAGTTTTCGCACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTTC 360
Db 329 CAGCCTGAGAGTTTTCGCACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTTC 388
Qy 361 GGCCACGAGCAAGGTTGGAATCAAA 387
Db 389 GGCCACGAGCAAGGTTGGAATCAAA 415
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without alignments!
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Prod. No. is the number of results that satisfy the condition
score greater than or equal to the score in the results table
and is derived by analysis of the total score profile

SUMMARY

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3	387	100.0	387	40	US-10-163-000-0
4	342.2	88.4	729	18	US-09-400-000-0
5	342.2	88.4	729	18	US-09-400-000-0
6	342.2	88.4	729	42	US-10-216-000-0
7	339	87.6	1106	4	US-09-292-053-5
8	339	87.6	1106	4	US-09-292-053-5
9	335.2	86.6	812	30	US-09-400-000-0
10	335.2	86.6	812	42	US-10-216-000-0
11	331.8	85.7	500	32	US-09-400-000-0
12	331.8	85.7	500	63	US-09-400-000-0
13	329.4	85.1	974	32	US-09-400-000-0
14	327.8	84.7	974	30	US-09-400-000-0
15	327.8	84.7	974	42	US-10-216-000-0
16	327	84.5	391	16	US-09-289-000-0
17	327	84.5	391	35	US-09-400-000-0
18	326.2	84.3	549	26	US-09-400-000-0
19	326.2	84.3	549	60	US-09-400-000-0
20	326.2	84.3	714	18	US-09-400-000-0
21	326.2	84.3	714	41	US-10-163-000-0

22 324.6 83.9 387 1 PCT-US99-09131-27 Sequence 27, Appl
23 324.6 83.9 387 17 US-09-300-970A-27 Sequence 27, Appl
24 324.6 83.9 387 34 US-09-905-243-27 Sequence 27, Appl
25 323 83.5 728 32 US-09-844-684-15 Sequence 15, Appl
26 323 83.5 728 38 US-10-040-244-15 Sequence 15, Appl
27 322.8 83.4 408 17 US-09-362-510-22815 Sequence 22815, A
28 322.8 83.4 408 34 US-09-362-510A-22815 Sequence 22815, A
29 322.8 83.4 408 37 US-09-904-013-22815 Sequence 22815, A
30 321.8 83.2 474 32 US-09-834-366-31 Sequence 31, Appl
31 321.8 83.2 474 63 US-09-197-873-31 Sequence 31, Appl
32 321.6 83.1 402 19 US-09-528-409-22604 Sequence 22604, A
33 321.6 83.1 402 35 US-09-933-524-22604 Sequence 22604, A
34 321.6 83.1 402 35 US-09-933-524A-22604 Sequence 22604, A
35 321.4 83.0 390 1 PCT-US99-09131-57 Sequence 57, Appl
36 321.4 83.0 390 17 US-09-300-970A-57 Sequence 57, Appl
37 321.4 83.0 390 34 US-09-905-243-57 Sequence 57, Appl
38 321.4 83.0 514 1 PCT-US02-02870-2025 Sequence 2025, Ap
39 321.4 83.0 514 39 US-10-066-543-2025 Sequence 2025, Ap
40 321.4 83.0 514 42 US-10-214-403-2025 Sequence 2025, Ap
C 41 321.4 83.0 537 1 PCT-US02-02870-186 Sequence 186, App
C 42 321.4 83.0 537 39 US-10-066-543-186 Sequence 186, App
C 43 321.4 83.0 537 42 US-10-214-403-186 Sequence 186, App
44 321.4 83.0 716 32 US-09-844-684-13 Sequence 13, Appl
45 321.4 83.0 716 38 US-10-040-244-13 Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-019-441-3
; Sequence 3, Application US/09019441
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 1..387
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..387
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-019-441-3
Query Match 100.0%; Score 387; DB 14; Length 387;
Best Local Similarity 100.0%; Pred. No. 5.9e-109; Indels 0; Gaps 0;
Matches 387; Conservative 0; Mismatches 0;
QY 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTCTGTGCTCTGGCTCCAGGTGCC 60
Db 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTCTGTGCTCTGGCTCCAGGTGCC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGCTATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGCTATCTGTAGGGGACAGA 120
QY 121 GTCAACATCACTTCAGGGCAAGTCAGACATTAAGGTATTATTTAAATTGTTATCAGCAG 180
Db 121 GTCAACATCACTTCAGGGCAAGTCAGACATTAAGGTATTATTTAAATTGTTATCAGCAG 180
QY 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGTC 240
Db 181 AAACAGGAAAGCTCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGTC 240
QY 241 CCATCAAGGTTACAGGGCAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCTG 300
Db 241 CCATCAAGGTTACAGGGCAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCTG 300
QY 301 CAGCTGAAGATTTTGGGACTTATTACTGTCTCAGAGTTTATAGTACCCCTCGGACGTTTC 360
Db 301 CAGCTGAAGATTTTGGGACTTATTACTGTCTCAGAGTTTATAGTACCCCTCGGACGTTTC 360
QY 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
Db 361 GGCCAAAGGACCAAGGTGGAAATCAAA 387
RESULT 2
US-09-292-053-5
; Sequence 5, Application US/09292053
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: NAKAMURA, TAKEHIKO
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
; FILE REFERENCE: THEREOF AS THERAPEUTICS
; FILE REFERENCE: 23522.0699
; CURRENT APPLICATION NUMBER: US/09/292,053
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 08/803,085
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(67)
; NAME/KEY: mat_peptide
; LOCATION: (67)..(387)
; NAME/KEY: CDS
; LOCATION: (1)..(387)
US-09-292-053-5
Query Match 100.0%; Score 387; DB 16; Length 387;
Best Local Similarity 100.0%; Pred. No. 5.9e-109; Indels 0; Gaps 0;
Matches 387; Conservative 0; Mismatches 0;


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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (201)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (792)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-760-479-405

      86.6%; Score 335.2; DB 30; Length 812;
Best Local Similarity 90.2%; Pred. No. 9,3e-93;
Matches 349; Conservative 7; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGTCCTCCCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGTGCC 60
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Db 41 ATGGACATGAGGTCCTCCCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCAGTGCC 100
   |||||

QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTCTGTCATCTCTAGGGGACAGA 120
   |||||
Db 101 AGATGTGACATGAGATGACCCAGTCTCCATCTTCCCTCTGTCATCTCTAGGGGACAGA 160
   |||||

QY 121 GTCCACCATCTTGCAGGCAAGTACGACATTAGGTATTATTTAAATTTGGTATCAGCAG 180
   |||||
Db 161 GTCCACCATCTTGCAGGCAAGTACGACATTAGGTATTATTTAAATTTGGTATCAGCAG 220
   |||||

QY 181 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTC 240
   |||||
Db 221 AAACAGGAAAGCTCTTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGTC 280
   |||||

QY 241 CCATCAAGTTTCAGCGGAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAAGCCCTG 300
   |||||
Db 281 CCATCAAGTTTCAGCGGAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAAGCCCTG 340
   |||||

QY 301 CAGCCTGAAGATTTTTCGCACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTT 360
   |||||
Db 341 CAACTGAAGATTTTTCGCACTTATTACTGTCTACAGAAATTCACCAATTCGGACGTTT 400
   |||||

QY 361 GCCCAAGGACCAAGTGAATCAAA 387
Db 401 GCCCAAGGACCAAGTGAATCAAA 427

RESULT 10
US-10-206-008-405
; Sequence 405, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ53CIN
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
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; PRIOR FILING DATE: 2000-09-01
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; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
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; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 44
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..498
; NAME/KEY: sig_peptide
; LOCATION: 28..93
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 13.6000003814697
; OTHER INFORMATION: seq LGLLLMLRGARC/DI
US-09-834-366-44

Query Match      85.7%; Score 331.8; DB 32; Length 500;
Best Local Similarity 86.0%; Pred. No. 8.8e-92;
Matches 333; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

QY      1  ATGGACATGAGGTCCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db      28  ATGGACATGAGGTCCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 87

QY      61  AGATGTGACATCCAGATGACCCAGTCCATCTCCCTGCTGTCATCTGTAGGGACAGA 120
Db      88  AGATGTGACATCCAGATGACCCAGTCCATCTCCCTGCTGTCATCTGTAGGGACAGA 147

QY      121  GTCACCATCACTTCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
Db      148  GTCACCATCACTTCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 207

QY      181  AAACAGGAAAGCTCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAAGTGGGTC 240
Db      208  AAACAGGAAAGCTCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAAGTGGGTC 267

QY      241  CCATCAAGTTTCAGGGGAGTGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTG 300
Db      268  CCATCAAGTTTCAGGGGAGTGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTG 327

QY      301  CAGCTGAAGATTTTGGGACTTATCTGTCACAGTTTATAGTACCCCTCGGACGTTTC 360
Db      328  CAGCTGAAGATTTTGGGACTTATCTGTCACAGTTTATAGTACCCCTCGGACGTTTC 387

QY      361  GGCCAAAGGACCAAGTGGAAATCAAA 387
Db      388  GGCCMRGGGACCAAGTGGARRTCARR 414
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RESULT 12
US-60-197-873-44
; Sequence 44, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81 US1 PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 44
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: 28..498
; NAME/KEY: sig_peptide
; LOCATION: 28..93
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 13.6000003814697
; OTHER INFORMATION: seq LGLLLMLRGARC/DI
US-60-197-873-44

Query Match      85.7%; Score 331.8; DB 63; Length 500;
Best Local Similarity 86.0%; Pred. No. 8.8e-92;
Matches 333; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

QY      1  ATGGACATGAGGTCCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 60
Db      28  ATGGACATGAGGTCCCCGCTCAGCTCCTGGGGCTCTTCTGCTCTGGCTCCAGGTGCC 87

QY      61  AGATGTGACATCCAGATGACCCAGTCCATCTTCTGCTGTCATCTGTAGGGACAGA 120
Db      88  AGATGTGACATCCAGATGACCCAGTCCATCTTCTGCTGTCATCTGTAGGGACAGA 147

QY      121  GTCACCATCACTTCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
Db      148  GTCACCATCACTTCGAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 207

QY      181  AAACAGGAAAGCTCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAAGTGGGTC 240
Db      208  AAACAGGAAAGCTCCTAAGCTCCTGATCTATCTGTCATCCAGTTTGCAAGTGGGTC 267

QY      241  CCATCAAGTTTCAGGGGAGTGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTG 300
Db      268  CCATCAAGTTTCAGGGGAGTGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTG 327

QY      301  CAGCTGAAGATTTTGGGACTTATCTGTCACAGTTTATAGTACCCCTCGGACGTTTC 360
Db      328  CAGCTGAAGATTTTGGGACTTATCTGTCACAGTTTATAGTACCCCTCGGACGTTTC 387

QY      361  GGCCAAAGGACCAAGTGGAAATCAAA 387
Db      388  GGCCMRGGGACCAAGTGGARRTCARR 414
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RESULT 13
US-09-859-053-29
; Sequence 29, Application US/09859053
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
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;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/249,299
;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/236,327
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/241,785
;; PRIOR FILING DATE: 2000-10-20
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;; PRIOR FILING DATE: 2000-11-01
;; PRIOR APPLICATION NUMBER: 60/225,268
;; PRIOR FILING DATE: 2000-08-14
;; PRIOR APPLICATION NUMBER: 60/236,368
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/251,856
;; PRIOR FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 60/251,868
;; PRIOR FILING DATE: 2000-12-08
;; PRIOR APPLICATION NUMBER: 60/229,344
;; PRIOR FILING DATE: 2000-09-01
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;; PRIOR APPLICATION NUMBER: 60/237,038
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;; PRIOR APPLICATION NUMBER: 60/237,040
;; PRIOR FILING DATE: 2000-10-02
;; PRIOR APPLICATION NUMBER: 60/240,960
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/239,935
;; PRIOR FILING DATE: 2000-10-13
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;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/241,787
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,474
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/246,532
;; PRIOR FILING DATE: 2000-11-08
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;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-08-22
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;; PRIOR FILING DATE: 2000-08-14
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;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 60/225,214
;; PRIOR FILING DATE: 2000-08-14

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;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,065

Query Match 84.7%; Score 327.8; DB 42; Length 974;
Best Local Similarity 90.4%; Pred. No. 2e-90;
Matches 350; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: PCT/US02/38550
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38550-113

Query Match 81.1%; Score 313.8; DB 2; Length 384;
Best Local Similarity 89.0%; Pred. No. 4.1e-93;
Matches 339; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 7 ATGAGGGTCCCGCTCAGCTCCCTGGGGTCTCTGCTCTGGCTCCCGAGTGCAGATGT 66
DB 1 ATGAGGGTCCCTGCTCAGCTCCCTGGGACTCTCTGCTCTGGCTCCCGAGTGCAGATGT 60

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTCGCATCTGTAGGGGACAGAGTCA 126
DB 61 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCGCATCTGTAGGAGACAGAGTCA 120

QY 127 ATCACTTCGAGGCAAGTCAGACATTAGGTATTTAAATTGGTATCAGCAAAACCA 186
DB 121 ATCACTTGGCGGGAGTCAGGCAATTTCAATTTATTTAGCTGGTATCAGCAAAACCA 180

QY 187 GGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCATAAGTGGGTCCTCATCA 246
DB 181 GGGAAAGTTCCTAAGCTCCTGATCTGTCATCCACTTTGCAATCAGGGTCCCATCT 240

QY 247 AGGTTACGGCGAGTGTCTGGGACAGATTTCACTCTCACCGTCAGAGCCTCGAGCCT 306
DB 241 CGGTTACGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGAGCCT 300

QY 307 GAAGATTTTGGCACTTATTTACTCTACAGTTTATAGTACCCCTCGAGCTTCGGCCAA 366
DB 301 GAAGATTTTGGCACTTATTTACTCTTAAAGTATTAACAGTGCCTGGACGTTTCGGCCAA 360

QY 367 GGGACCAAGGTGGAATCAAA 387
DB 361 GGGACCAAGGTGGAATCAAA 381

RESULT 7
US-10-309-762-113
; Sequence 113, Application US/10309762
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-113

Query Match 81.1%; Score 313.8; DB 14; Length 384;
Best Local Similarity 89.0%; Pred. No. 4.1e-93;
Matches 339; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 7 ATGAGGGTCCCGCTCAGCTCCCTGGGGTCTCTTCTGCTCTGGCTCCCGAGTGCAGATGT 66
DB 1 ATGAGGGTCCCTGCTCAGCTCCCTGGGACTCTCTGCTCTGGCTCCCGAGTGCAGATGT 60

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTCGCATCTGTAGGGGACAGAGTCA 126
DB 61 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCACTCTGTAGGAGACAGAGTCA 120

QY 127 ATCACTTCGAGGCAAGTCAGGACATTAGGTATTTAAATTGGTATCAGCAAAACCA 186
DB 121 ATCACTTGGCGGGAGTCAGGCAATTTCAATTTATTTAGCTGGTATCAGCAAAACCA 180

QY 187 GGAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCATAAGTGGGTCCTCATCA 246
DB 181 GGGAAAGTTCCTAAGCTCCTGATCTGTCATCCACTTTGCAATCAGGGTCCCATCT 240

QY 247 AGGTTACGGCGAGTGTCTGGGACAGATTTCACTCTCACCGTCAGAGCCTCGAGCCT 306
DB 241 CGGTTACGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGAGCCT 300

QY 307 GAAGATTTTGGCACTTATTTACTCTACAGTTTATAGTACCCCTCGAGCTTCGGCCAA 366
DB 301 GAAGATTTTGGCACTTATTTACTCTTAAAGTATTAACAGTGCCTGGACGTTTCGGCCAA 360

QY 367 GGGACCAAGGTGGAATCAAA 387
DB 361 GGGACCAAGGTGGAATCAAA 381

RESULT 8
US-10-170-235-5868
; Sequence 5868, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 5868
; LENGTH: 406
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-5868

Query Match 80.8%; Score 312.6; DB 15; Length 406;
Best Local Similarity 90.7%; Pred. No. 1e-92;
Matches 333; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCGAGTGC 60
DB 29 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTTCTGCTCTGGCTCCCGAGTGC 88

QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTCGCATCTGTAGGGGACAGA 120
DB 89 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGCTCGCATCTGTAGGAGACAGA 148

QY 121 GTCACCATCACTTCGAGGGCAAGTCAGGACATTAGGTATTTAAATTGGTATCAGCAG 180
DB 149 GTCACCATCACTTCGCGGGCAAGTCAGAGCATTTAGCAGTATTTAAATTTGGTATCAGCAG 208

QY 181 AAACACAGAAAGCTCCTAAGCTCTGATCTATGTTGCATCCAGTTTGCATAAGTGGGTC 240
DB 209 AAACACAGAAAGCTCCTAAGCTCTGATCTATGCTGATCCAGTTTGCATAAGTGGGTC 268

QY 241 CCATCAAGGTTTCAGCGGAGTGGATCTGGGACAGATTTCACTCTCACCGTCAGAGCCTG 300
DB 269 CCATCAAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG 328

QY 301 CAGCCTGAAGATTTTGGCACTTATTTACTGTCTACAGTTTATAGTACCCCTCGGACGTTTC 360
DB 329 CAACCTGAAGATTTTGGCACTTATTTACTGTCTCAACAGAGTTACAGTACCCCTCCACACGTC 388

QY 307 GAAGATTTCGACCTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCGTTGGCCAA 366
|||||
Db 301 GAAGATTTCGAACTTACTACTGTCAACAGAGTTACAGTTCCCTATTACCTTTTGGCCCT 360
|||||
QY 367 GGGACCAAGGTGGAATCAAA 387
|||||
Db 361 GGGACCAAGTGGATATCAAA 381
|||||

RESULT 12

US-10-309-762-115

; Sequence 115, Application US/10309762

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian

; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN

; FILE REFERENCE: ABGENIX.027A

; CURRENT APPLICATION NUMBER: US/10/309,762

; CURRENT FILING DATE: 2002-12-02

; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 115

; LENGTH: 384

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-309-762-115

Query Match 79.8%; Score 309; DB 14; Length 384;

Best Local Similarity 88.2%; Pred. No. 1.6e-91;

Matches 336; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 7 ATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGCTCCAGGTGCCAGATGT 66
|||||
Db 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGCTCCAGGTGCCAGATGT 60
|||||

QY 67 GATATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGACAGAGTCACC 126
|||||
Db 61 GATATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGACAGAGTCACC 120
|||||

QY 127 ATCACTTGCAGGCAAGTACAGACATTAGTATTATTAATTGGTATCAGCAGAAACA 186
|||||
Db 121 ATCACTTGCAGGCAAGTACAGACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACA 180
|||||

QY 187 GGAAAGCTCTTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAGTGGGTCCCATCA 246
|||||
Db 181 GGAAAGCTCTTAAGCTCTGATCTATCTATCTGATCCATTTGGAGTGGGTCCCATCA 240
|||||

QY 247 AGGTTCCAGGCGAGTGGATCTGGGACAGATTCCTCTCACCTCAGCAGCCTCGAGCCT 306
|||||
Db 241 AGGTTCCAGTGGCAGTGGATCTGGGACAGATTCCTCTCACCTCAGCAGCCTCGAACT 300
|||||

QY 307 GAAGATTTTCGACCTTATTACTGTCTACAGTTTATAGTACCCCTCGAGCGTTGGCCAA 366
|||||
Db 301 GAAGATTTTCGAACTTACTACTGTCAACAGAGTTACAGTTCCCTATTCTACTTTGGCCCT 360
|||||

QY 367 GGGACCAAGGTGGAATCAAA 387
|||||
Db 361 GGGACCAAGTGGATATCAAA 381
|||||

RESULT 13

PCT-US03-00657-7

; Sequence 7, Application PC/TUS0300657

; GENERAL INFORMATION:

; APPLICANT: Hansen, Rhonda

; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

; TITLE OF INVENTION: IN CANCEROUS BREAST CELLS AND THEIR METHODS OF USE

; FILE REFERENCE: 2300-17767WO

; CURRENT APPLICATION NUMBER: PCT/US03/00657
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/345,637
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-00657-7

Query Match 79.7%; Score 308.6; DB 2; Length 548;

Best Local Similarity 87.3%; Pred. No. 2.5e-91;

Matches 338; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGCTCCAGGTGCC 60
|||||
Db 7 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCCTTCTGCTCTGCTCCAGGTGCC 66
|||||

QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGACAGA 120
|||||
Db 67 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGACAGA 126
|||||

QY 121 GTCAACATCACTTGCAGGCAAGTACAGACATTAGTATTATTTAAATTGGTATCAGCAG 180
|||||
Db 127 GTCAACATCGTTGCCGGGCAAGTACAGACATTAGTATTATTTAAATTGGTATCAGCAG 186
|||||

QY 181 AAACAGGAAAGCTCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGTC 240
|||||
Db 187 AAACAGGAAAGCTCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAGAGTGGGTC 246
|||||

QY 241 CCATCAAGGTTTCAGGCGCAGTGGATCTGGGACAGATTCCTCTCACCTCAGCAGCCTG 300
|||||
Db 247 CCATCAAGGTTTCAGGCGCAGTGGATCTGGGACAGATTCCTCTCACCTCAGCAGCCTG 306
|||||

QY 301 CAGCTCAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCAGTTC 360
|||||
Db 307 CAACCTGAAGATTAGCAACTTACTACTGTCAACAGGGTACAGTACACCTGGCACCTTC 366
|||||

QY 361 GGCCAAAGGCAAGGTGGAAATCAAA 387
|||||
Db 367 GGCCAAAGGCAAGGTGGAAATTAAT 393
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RESULT 14

PCT-US02-33944-20

; Sequence 20, Application PC/TUS0233944

; GENERAL INFORMATION:

; APPLICANT: PSMA DEVELOPMENT COMPANY, L.L.C.

; APPLICANT: MADON, Paul J.

; APPLICANT: DONOVAN, Gerald P.

; APPLICANT: OLSON, William C.

; APPLICANT: SCHLKE, Norbert

; APPLICANT: GARDNER, Jason

; APPLICANT: MA, Dangshe

; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS

; FILE REFERENCE: P00453.70005.WO

; CURRENT APPLICATION NUMBER: PCT/US02/33944

; CURRENT FILING DATE: 2002-10-23

; PRIOR APPLICATION NUMBER: US 60/335,215

; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: US 60/362,747

; PRIOR FILING DATE: 2001-03-07

; PRIOR APPLICATION NUMBER: US 60/____, ____

; PRIOR FILING DATE: 2002-09-20

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 463

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

Best Local Similarity 100.0%; Pred. No. 9.8e-113;		
Matches 387;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	ATGACATGAGGTCCTCCCGTCAGCTCCTGGGGCTCTTCTGTCTCGCTCCCGACGTGCC 60
Db	1	ATGACATGAGGTCCTCCCGTCAGCTCCTGGGGCTCTTCTGTCTCGCTCCCGACGTGCC 60
Qy	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db	61	AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Qy	121	GTCAACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 180
Db	121	GTCAACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG 180
Qy	181	AAACCAGGAAAGTCTCTAAGTCTCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 240
Db	181	AAACCAGGAAAGTCTCTAAGTCTCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 240
Qy	241	CCATCAAGTTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCGTCAGCAGCGCTG 300
Db	241	CCATCAAGTTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCGTCAGCAGCGCTG 300
Qy	301	CAGCCTGAAGATTTTGGCGACTTATTACTGTCTACAGGTTTTATAGTACCCCTCGGACGTTTC 360
Db	301	CAGCCTGAAGATTTTGGCGACTTATTACTGTCTACAGGTTTTATAGTACCCCTCGGACGTTTC 360
Qy	361	GGCCAGGGGACCAAGGTGGAAATCAAA 387
Db	361	GGCCAGGGGACCAAGGTGGAAATCAAA 387

RESULT 2

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US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 641377
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCLACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Mandy"
US-09-343-485A-3

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Qy	121	GTCCACCATCATTGCGAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG	180
Db	7665	GTCCACATCATTGCGAGGCAAGTCAGGACATTAGGTATTATTAAATTTGGTATCAGCAG	7724
Qy	181	AAACCAAGGAAAGCTCCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAAGTGGGTC	240
Db	7725	AAACCAAGGAAAGCTCCTTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAAGTGGGTC	7784
Qy	241	CCATCAAGGTTTCAGCGCGAGTCGATCTGGGACAGAGTTTCACCTCTCACCGTCAGCAGCCTG	300
Db	7785	CCATCAAGGTTTCAGCGCGAGTCGATCTGGGACAGAGTTTCACCTCTCACCGTCAGCAGCCTG	7844
Qy	301	CAGCCTGAAGATTTTCGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGGACGTTTC	360
Db	7845	CAGCCTGAAGATTTTCGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGGACGTTTC	7904
Qy	361	GGCCAAAGGACCAAGGTGGAATCAA	387
Db	7905	GGCCAAAGGACCAAGGTGGAATCAA	7931
RESULT 3			
US-09-042-353-358			
; Sequence 358, Application US/09042353			
; Patent No. 6255458			
; GENERAL INFORMATION:			
; APPLICANT: Lonberg, Nils			
; APPLICANT: Kay, Robert M.			
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for			
; TITLE OF INVENTION: Producing Heterologous Antibodies			
; NUMBER OF SEQUENCES: 421			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94111-3834			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/042,353			
; FILING DATE: 13-MAR-1998			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/810,279			
; FILING DATE: 17-DEC-1991			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/853,408			
; FILING DATE: 18-MAR-1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/904,068			
; FILING DATE: 23-JUN-1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/990,860			
; FILING DATE: 16-DEC-1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/053,131			
; FILING DATE: 26-APR-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/096,762			
; FILING DATE: 22-JUL-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/155,301			
; FILING DATE: 18-NOV-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/161,739			
; FILING DATE: 03-DEC-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/165,699			


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; NAME/KEY: CDS
; LOCATION: 1..705
US-08-770-057-16

Query Match      78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCGCTCAGCTCTGGGCTCTTCTGCTGCTCCAGGTGCCAGATGT 66
Db 1 ATGGAGACCCCTGCTCAGCTCTGGGCTCTTCTGCTGCTCCAGGTGCCAGATGT 60

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGAGTCACC 126
Db 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGAGTCACC 120

QY 127 ATCACTTGGAGGCAAGTCAGACATTTAGGTATTTAAATTTGGTATCAGCAGAAACCA 186
Db 121 ATCACTTGGAGGCAAGTCAGACATTTAGGTATTTAAATTTGGTATCAGCAGAAACCA 180

QY 187 GGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTGCRAAGTGGGTCCCATCA 246
Db 181 GGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTGCRAAGTGGGTCCCATCA 240

QY 247 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
Db 241 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAACAGTCTGCAACT 300

QY 307 GAAGATTTTGCACCTTATCTGCTACAGGTTTATAGTACCCCTCGGAGCGTTGGGCAA 366
Db 301 GAAGATTTTGCACCTTATCTGCTACAGGTTTATAGTACCCCTCGGAGCGTTGGGCAA 360

QY 367 GGGACCAAGTGGAAATCAAA 387
Db 361 GGGACCAAGTGGAAATCAAA 381

RESULT 15
US-09-335-697B-16
; Sequence 16, Application US/09335697B
; Patent No. 6200804
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; CHAMAT, Soulaime Salim
; PAN, Li-Zhen
; WALSH, Edward E.
; HEARD, Cheryl Janne
; NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/335,697B
; FILING DATE: 06-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/770,057
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.

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; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-335-697B-16

Query Match      78.6%; Score 304.2; DB 4; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.5e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCGCTCAGCTCTGGGCTCTTCTGCTGCTCCAGGTGCCAGATGT 66
Db 1 ATGGAGACCCCTGCTCAGCTCTGGGCTCTTCTGCTGCTCCAGGTGCCAGATGT 60

QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGAGTCACC 126
Db 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGTCATCTGTAGGGGACAGAGTCACC 120

QY 127 ATCACTTGGAGGCAAGTCAGGACATTTAGGTATTTAAATTTGGTATCAGCAGAAACCA 186
Db 121 ATCACTTGGAGGCAAGTCAGGACATTTAGGTATTTAAATTTGGTATCAGCAGAAACCA 180

QY 187 GGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTGCRAAGTGGGTCCCATCA 246
Db 181 GGAAAGCTCCTAAGCTCTGATCTATGTCATCCAGTTTGCRAAGTGGGTCCCATCA 240

QY 247 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
Db 241 AGGTTTCAGCGGCGAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAACAGTCTGCAACT 300

QY 307 GAAGATTTTGCACCTTATCTGCTACAGGTTTATAGTACCCCTCGGAGCGTTGGGCAA 366
Db 301 GAAGATTTTGCACCTTATCTGCTACAGGTTTATAGTACCCCTCGGAGCGTTGGGCAA 360

QY 367 GGGACCAAGTGGAAATCAAA 387
Db 361 GGGACCAAGTGGAAATCAAA 381

Search completed: July 15, 2003, 08:30:15
Job time : 31.5084 secs

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TITLE Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHV1-IGHV7 subgroups

JOURNAL Immunogenetics 53 (10-11), 815-820 (2002)

MEDLINE 21850497

PUBMED 11862381

REFERENCE 2 (bases 1 to 429)

AUTHORS Scinicariello,F., Jayashankar,L. and Attanasio,R.

TITLE Direct Submission

JOURNAL Submitted (04-SEP-2001) Department of Biology, Georgia State University, PO BOX 4010, Atlanta, GA 30302, USA

FEATURES Location/Qualifiers

source 1..429

1..429

/organism="Papio cynocephalus anubis"

/sub_species="anubis"

/db_xref="taxon:9555"

/clone="VH3-d3"

1..429

/codon_start=1

/product="immunoglobulin heavy chain variable region"

/protein_id="AAL96421.1"

/db_xref="GI:19744272"

/translation="MEFGLSWFLVALLKGVQGEVQLVESGGGLAKPGGSLRLSCAAS GFTFSDYMDVWRQAPGKLEWVSRIPTGSGTWYADSVKGRFTISRNAKNTLYLQNM SURAEDEVYICARDRDSNMGFDYWGQGLVLTSSASAS"

BASE COUNT 87 a 107 c 141 g 94 t

ORIGIN

Query Match 74.9%; Score 307.8; DB 9; Length 429;

Best Local Similarity 88.7%; Pred. No. 1.1e-72;

Matches 375; Conservative 0; Mismatches 27; Indels 21; Gaps 3;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTGAAGGTTCTCCAGTGTGAG 60

Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTGAAGGTTCTCCAGGTTGAG 60

QY 61 GTGCAGCTGTGGAGTCTGGGGGGCGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120

Db 61 GTGCAGCTGTGGAGTCTGGGGGGCGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120

QY 121 TCGCAGCTCTCGGGTTTCAGGTTTCACTTCAATACTACTACATGAGTGGTCCGCCAG 180

Db 121 TCGCAGCTCTCGG-----GATTCACCTTCAGTGACTACTACATGAGTGGTCCGCCAG 174

QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTATCCCATGG 240

Db 175 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACTAT---TAATACTGGTGGCGACATGG 231

QY 241 TACGAGACTCTGTAAGGCGAGATTCACCATCTCCAGAGAGACGCCCAACACACTG 300

Db 232 TACGAGACTCTGTAAGGCGGATTCACCATCTCCAGAGAGACGCCCAACACACTG 291

QY 301 TTTCTTCAAATGAACAGCTGAGAGTGGAGTGGGTCTCACTATTAGTGGTCTTATTACTGTCCGAG---- 356

Db 292 TATCTTCAAATGAACAGCTGAGAGTGGAGTGGGTCTCACTATTAGTGGCGAGAT 351

QY 357 -----CTTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTTGGTCAACCGTCTCC 408

Db 352 CGAAGGCGACAGTAACCTGGGGGTTTGACTACTCTGGGCCAGGGAGTCTTGGTCAACCGTCTCC 411

QY 409 TCA 411

Db 412 TCA 414

RESULT 2

HUMIGHADC 405 bp mRNA linear PRI 09-NOV-1994

LOCUS Human Ig rearranged gamma-chain mRNA V-region, 5' end of cds (from clone S1P15).

DEFINITION

ACCESSION L06912

VERSION L06912.1 GI:185008

KEYWORDS V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain; processed gene.

1

SOURCE Homo sapiens (tissue library: BC) Female Adult Synovium cDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 405)

AUTHORS Bridges,S.L. Jr., Lee,S.K., Koopman,W.J. and Schroeder,H.W. Jr.

TITLE Analysis of immunoglobulin gamma heavy chain expression in synovial tissue of a patient with rheumatoid arthritis

JOURNAL Arthritis Rheum. 36 (5), 631-641 (1993)

MEDLINE 93256941

PUBMED 8489540

FEATURES Location/Qualifiers

source 1..405

1..405

/organism="Homo sapiens"

/db_xref="taxon:9606"

/map="14q32.33"

/sex="Female"

/cell_type="B cell"

/tissue_type="Synovium"

/dev_stage="Adult"

/tissue_lib="BC"

1..405

/gene="IGHV@"

1..405

/gene="IGHV@"

/codon_start=1

/product="immunoglobulin gamma-chain"

/protein_id="AA52798.1"

/db_xref="GI:185009"

/translation="MEFGLSWFLVALLKGVQGEVQLVESGGGLVLPKGGSLRLSCAAS GFTPSDYMTWIRQAPGKLEWVSIRPTGNIIVYADSVKGRFTISRDNKNSLYLQM NSLRAPETAIIYCAARGVETAAYWQGSLTVTSS"

58..405

/gene="IGHV@"

/note="G00-128-528; putative"

BASE COUNT 89 a 98 c 124 g 94 t

ORIGIN

Query Match 71.3%; Score 293; DB 9; Length 405;

Best Local Similarity 83.9%; Pred. No. 1.1e-68;

Matches 345; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTGAAGGTTCCAGTGTGAG 60

Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTGAAGGTTCCAGTGTGAG 60

QY 61 GTGCAGCTGTGGAGTCTGGGGGGCGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120

Db 61 GTGCAGCTGTGGAGTCTGGGGGGCGCTTGGTCAAGCTGGAGGTTCCCTGAGACTCTCC 120

QY 121 TGGCAGCTCTCGGGTTTCAGGTTTCACTTCAATACTACTACATGAGTGGTCCGCCAG 180

Db 121 TGTGAGCCTCTG-----GAATCACCTTCAGTGACTACTACATGAGTGGTCCGCCAG 174

QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACTATTAGTAGTGGTATCCCATGG 240

Db 175 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACTATTAGTGGTATCCCATGATATATAC 234

QY 241 TACGAGACTCTGTAAGGCGAGATTCACCATCTCCAGAGAGAACGCCCAACACACTG 300

Db 235 TACGAGACTCTGTAAGGCGCGATTCAACCACTCCAGGGGACACGCCCAAGAACTACTG 294

QY 301 TTTCTTCAAATGAACAGCTGAGAGTGGAGTGGGTCTTATTACTGTCCGAGCTTG 360

Db 295 TATCTGAAAATGAACAGCTGAGAGCGGAGACACGCCCATATATTACTGTCCGAGAGG 354

QY 361 ACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTTGGTCAACCGTCTCTCA 411

Db 355 GTTGAGAGCGGGCGCTACTTGGGGCCAGGAAACCTTGTGTCACCGTCTCTCA 405


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QY      61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120
D      84 GTGCAGCTTGGAGTCTGGGGAGGCTTGGTACAGCCCTGGGGGTCCCTGAGACTCTCC 143
QY     121 TGCAGAGCTCCGGGTTACAGTTACCTTCAATAACTACTAATGAGACTGGTCCGCCAG 180
D      144 TGTGACGCTCTG-----GATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAG 197
QY     181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCATATGG 240
D      198 GCTCAGGGAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCAGATAC 257
QY     241 TACGAGACTCTCGTGAAGGCGAGATTCCACATCTCCAGAGAGAAACGCAACACACTG 300
D      258 TACGAGACTCTCGTGAAGGCGGTTCCACATCTCCAGAGAGAAATCCAGAGACGCTG 317
QY     301 TTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA----- 355
D      318 TATCTGCAATGAACAGCTGAGAGCGGAGGACACGGCGGTATATTACTGTGCGAAGAT 377
QY     356 ----GCTTCACTACAGGCTCACTCTCGGGCCAGGAGTCTCGTCAACGCTCTCCTCA 411
D      378 GCGGCTGGGTTCGGGGTTGACTACTGGGGCCAGGGAACCTGGTCAACGCTCTCCTCA 437

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RESULT 5
HSBEL20          415 bp      mRNA      linear      PRI 29-FEB-1996
LOCUS            H.sapiens rearranged VDJ region (BEL20).
DEFINITION       H.sapiens rearranged VDJ region (BEL20).
ACCESSION        X81725
VERSION          X81725.1 GI:1212930
KEYWORDS         diversity region; immunoglobulin heavy chain; joining region;
                 variable region; VH-3 family.
SOURCE            Homo sapiens.
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1 (bases 1 to 415)
AUTHORS          Milili,M., Schiff,C., Fougereau,M. and Tonnelle,C.
TITLE            The VDJ repertoire expressed in human preB cells reflects the
                 selection of bona fide heavy chains
JOURNAL          Eur. J. Immunol. 26 (1), 63-69 (1996)
MEDLINE          96152725
PUBMED           8566085
REFERENCE        2 (bases 1 to 415)
AUTHORS          Tonnelle,C.
TITLE            Direct Submission
JOURNAL          Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie
                 Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE
COMMENT          Related sequences: X65741, X65983 to X65920.
FEATURES         Location/Qualifiers
                 1..415
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /chromosome="14"
                 /clone="BEL 20"
                 /cell_type="pre B-lymphocytes"
                 /tissue_type="bone marrow"
                 /clone_lib="BEL"
                 /rearranged
                 1..57
                 /product="immunoglobulin heavy chain V region"
                 58..345
                 /product="immunoglobulin heavy chain D segment"
                 346..372
                 /product="immunoglobulin heavy chain D segment"
                 373..415
                 /product="immunoglobulin heavy chain J segment"
BASE COUNT      91 a 99 c 122 g 103 t
ORIGIN

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Query Match      68.8%; Score 282.6; DB 9; Length 415;
Best Local Similarity 83.4%; Pred. No. 7.2e-66;

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Matches 351; Conservative 0; Mismatches 54; Indels 16; Gaps 2;
QY      1 'ATGAGATTGGGCTGAGCTGGGTTTCTCTGCTTCTCTTTTAAAGGTGTCAGTGTGAG 60
D      1 'ATGAGATTGGGCTGAGCTGGGTTTCTCTGCTTCTCTTTTAAAGGTGTCAGTGTGAG 60
QY     61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120
D      61 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGAGGGTCCCTGAGACTCTCC 120
QY     121 TGCAGAGCTCCGGGTTACAGTTCCCTTCAATTAATCTACATGAGACTGGGTCCGCCAG 180
D      121 TGTGAGCCTCTG-----GATTACCTTCACTAGTATTATGAATCAACTGGGTCCGCCAG 174
QY     181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATCCCATATGG 240
D      175 CCTCAGGGAAGGGCTGGAGTGGGTTCATACATTAGTAGTGGTATGACCATATAC 234
QY     241 TACGAGACTCTCGTGAAGGCGAGATTCCACATCTCCAGAGAGAAACGCAACACACTG 300
D      235 TACGAGACTCTCGTGAAGGCGGATTCCACATCTCCAGAGAGAAACGCAACACTG 294
QY     301 TTCTTCAATGAACAGCTGAGAGCTGAGAGACACGGCTGTCTATTACTGTGCGAGCTTG 360
D      295 TATCTGCAATGAACAGCTGAGAGCGGAGACACGGCTGTTTATTACTGTCAAAACCTAG 354
QY     361 ACTA-----CAGGGTCTGACTCTCTGGGGCCAGGAGTCTCTGGTCAACGCTCTCCTC 410
D      355 AGGAAGTCCCGGAGCTCTTTTGACTACTGGGGCAGGGAACCTCTGGTCAACCTCTCCTC 414
QY     411 A 411
D      415 A 415

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RESULT 6
HSBEL28          411 bp      mRNA      linear      PRI 29-FEB-1996
LOCUS            H.sapiens rearranged VDJ region (BEL28).
DEFINITION       H.sapiens rearranged VDJ region (BEL28).
ACCESSION        X81726
VERSION          X81726.1 GI:1212931
KEYWORDS         diversity region; immunoglobulin heavy chain; joining region;
                 variable region; VH-3 family.
SOURCE            Homo sapiens.
ORGANISM         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1 (bases 1 to 411)
AUTHORS          Milili,M., Schiff,C., Fougereau,M. and Tonnelle,C.
TITLE            The VDJ repertoire expressed in human preB cells reflects the
                 selection of bona fide heavy chains
JOURNAL          Eur. J. Immunol. 26 (1), 63-69 (1996)
MEDLINE          96152725
PUBMED           8566085
REFERENCE        2 (bases 1 to 411)
AUTHORS          Tonnelle,C.
TITLE            Direct Submission
JOURNAL          Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie
                 Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE
COMMENT          Related sequences: X65741, X65883 to X65920.
FEATURES         Location/Qualifiers
                 1..411
                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /chromosome="14"
                 /clone="BEL 28"
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                 /tissue_type="bone marrow"
                 /clone_lib="BEL"
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sig_peptide      1..57
V_region          58..352

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1. .423
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q32.33"
/clone="Xu-57"
/cell_type="peripheral B lymphocyte"
/tissue_type="blood"
/notes="from young repertoire Xu"
1. .>423
/gene="IGH"
1. .>423
/gene="IGH"
/codon_start=1
/product="immunoglobulin heavy chain variable region"
/protein_id="AAC18322.1"
/db_xref="GI:3171043"
GFTFSSYEMNVRQAPGKLEWVSIVSSGSTIYYADSVKGRFTISRDNAKNSLYLQM
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sig_peptide
1. .57
/gene="IGH"
58. .>423
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BASE COUNT      92 a      134 g      106 t
ORIGIN
Query Match      67.9%; Score 279.2; DB 9; Length 423;
Best Local Similarity 82.6%; Pred. No. 6e-65;
Matches 352; Conservative 0; Mismatches 53; Indels 21; Gaps 2;

Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCTTTGTTCTCTTTTGAAGGTGTCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTGCTGCTGGGTTTTCTTTGTTCTATTTTGAAGGTGTCAGTGTGAG 60

Qy 61 GTGCAGCTGTGGAGTCTGTGGGGCGGCTTGGCAAGCCTGGGGGTCTCCTGAGACTCTCC 120
Db 61 GTGCAGCTGTGGAGTCTGTGGGGCGGCTTGGTACAGCCTGGAGGCTCCTGAGACTCTCC 120

Qy 121 TCCGAGCTCCGGGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 180
Db 121 TGTGAGCTCTG-----GATTCACCTTCAGTAGTTATGAATGAATGAATGAATGAATGAAT 174

Qy 181 GCTCAGGCGAGGGCTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 240
Db 175 GCTCAGGCGAGGGCTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 234

Qy 241 TACGAGACTCTCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 TACGAGACTCTGTGAAGGCGGATTCACCATCTCCAGAGAGAACGCCAACAACTCACTG 294

Qy 301 TTTCTTCAATCAACAGCTGAGCTGAGGACGCGTGTCTATTACTGTGCG----- 354
Db 295 TATCTGCAATGAACAGCTGAGCGCGAGGACGCGTGTCTATTACTGTGCGAGAGAT 354

Qy 355 -----AGCTTGAATCAAGGCTGTGACTCTGGGGCGAGGAGTCTGTGTCAACCTC 405
Db 355 TTATGACGAGCTGTGATTATGAGGAGACTACTGGGGCGAGGAACTCTGTGTCAACCTC 414

Qy 406 TCCTCA 411
Db 415 TCCTCA 420

RESULT 9
AF062260
LOCUS
DEFINITION
Homo sapiens clone Xu-15 immunoglobulin heavy chain variable region
(IGH) mRNA, partial cds.
ACCESSION
AF062260
VERSION
AF062260.1 GI:3170986
KEYWORDS
Homo sapiens.

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ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 402)
AUTHORS        Wang, X. and Stollar, B.D.
TITLE          Immunoglobulin VH gene expression in human aging
JOURNAL        Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE        99459182
PUBMED         10527689
REFERENCE      2 (bases 1 to 402)
AUTHORS        Wang, X. and Stollar, B.D.
TITLE          Direct Submission
JOURNAL        Submitted (24-APR-1998) Biochemistry Department, Tufts University
FEATURES       Location/Qualifiers
source         1. .402
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="14"
               /map="14q32.33"
               /clone="Xu-15"
               /cell_type="peripheral B lymphocyte"
               /tissue_type="blood"
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               /protein_id="AAC18296.1"
               /db_xref="GI:3170987"
               /translation="MEFGLSLFLVAILKGVCVOLLESGLVOPGSLRLSCAAS
               GFTFSSYAMSWVRQAPGKLEWVSIVSSGSTIYYADSVKGRFTISRDNSKNTLYLQM
               NSLRAEDTAVYYCAKGGVYWGQGLTVTVSSG"

sig_peptide    1. .57
               /gene="IGH"
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BASE COUNT     80 a     93 c     132 g     97 t
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Query Match      67.9%; Score 279; DB 9; Length 402;
Best Local Similarity 83.7%; Pred. No. 6.8e-65;
Matches 344; Conservative 0; Mismatches 55; Indels 12; Gaps 2;

Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCTTTGTTCTCTTTTGAAGGTGTCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCTTTGTTCTATTTTAAAGGTGTCAGTGTGAG 60

Qy 61 GTGCAGCTGTGGAGTCTGTGGGGCGGCTTGGCAAGCCTGGGGGTCTCCTGAGACTCTCC 120
Db 61 GTGCAGCTGTGGAGTCTGTGGGGCGGCTTGGTACAGCCTGGGGGTCTCCTGAGACTCTCC 120

Qy 121 TGCAGCCTCCCGGGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 180
Db 121 TGTGAGCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGTCCGCCAG 174

Qy 181 GCTCAGGCGAGGGCTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 240
Db 175 GCTCAGGCGAGGGCTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 234

Qy 241 TACGAGACTCTCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 TACGAGACTCTGTGAAGGCGGATTCACCATCTCCAGAGAGAACGCCAACAACTCACTG 294

Qy 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGCGAGCTG 360
Db 295 TATCTGCAATGAACAGCTGAGCGCGAGGACACGCGTGTCTATTACTGTGCG-----G 348

Qy 361 ACTACAGGCTGTGACTCTCTGGGGCGAGGAGTCTGTGTCAACCTCTCTCTCA 411
Db 349 AAGATGGTGTGTCTACTTGGGGCGAGGAACTCTGTGTCAACCTCTCTCTCA 399

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RESULT 12
LOCUS HSVHIC10 408 bp mRNA linear PRI 15-FEB-1996
DEFINITION H.sapiens mRNA for immunoglobulin heavy chain V-region (clone
CDN3IC10).
ACCESSION Z47226
VERSION 247226.1 GI:1197316
KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 113)
AUTHORS Demaison,C., David,D., Letourneur,F., Zouali,M., Saragosti,S. and
Theze,J.
TITLE A cDNA/anchor-PCR approach to analyse the human VH gene repertoire
expressed by peripheral CD19+ B cells reveals a strong bias usage
of immunoglobulin heavy chain variable region.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 408)
AUTHORS Demaison,C.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1994) Christophe Demaison, Immunologie, Unite
d'Immunogenetique Cellulaire-Institut Pasteur, 25, rue du Docteur
Roux, Paris, 75015, FRANCE
REFERENCE 3 (bases 1 to 408)
AUTHORS Demaison,C., David,D., Letourneur,F., Theze,J., Saragosti,S. and
Zouali,M.
TITLE Analysis of human VH gene repertoire expression in peripheral CD19+
B cells
JOURNAL Immunogenetics 42 (5), 342-352 (1995)
MEDLINE 96006568
PUBMED 7590967
FEATURES
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Location/Qualifiers
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/clone="CDN3IC10"
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/tissue_type="peripheral blood lymphocyte"
/dev_stage="adult"
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58..408
/product="immunoglobulin variable region"
BASE COUNT 83 a 101 c 129 g 95 t
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Best Local Similarity 83.1%; Pred. No. 9.9e-65;
Matches 344; Conservative 0; Mismatches 61; Indels 9; Gaps 2;
QY 1 ATGGAGTTGGCTGAGCTGGGTTTCTTCTCTCTTTTGAAGGTGTCAGGTGAG 60
DB 1 ATGGAGTTGGCTGAGCTGGGTTTCTTCTCTCTTTTGAAGGTGTCAGGTGAG 60
QY 61 GTGCAGCTGCTGGGTTGAGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 120
DB 61 GTGCAGCTGCTGGGTTGAGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 120
QY 121 TCGCAGCTGCTGGGTTGAGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 180
DB 121 TCGCAGCTGCTGGGTTGAGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 180
QY 181 GCTCAGGCGAGGGCTGGAGTGGGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 240
DB 175 GCTCAGGCGAGGGCTGGAGTGGGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 234
QY 241 TACGAGACTCCGTTGAAGGCGAGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 300
DB 235 TACGAGACTCCGTTGAAGGCGAGTTTCAATTAACCTACATGAGTGGGTGCGCCAG 294
QY 301 TTCTTCAAATGAACAGCTGAGAGTGGAGGACAGGCTGTCTATTACTGTGCGAGCTTG 360

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DB 295 TATCTGCAATGAACAGCTGAGAGCGGACACGCGCTATATTACTGTGCAAGAT 354
QY 361 ACTACAGGTC---TGACTCTCTGGGCGCAGGAGTCTCTGGTCAACGCTCTCTCA 411
DB 355 GCCCCTTGAGCCGAGACTACTGGGCGCAGGAAACCTGTGGTCAACGCTCTCTCA 408

RESULT 13
LOCUS HUMIGHCXE 470 bp mRNA linear PRI 11-JUL-1995
DEFINITION Human fecal Ig heavy chain variable region (clone M43) mRNA,
partial cds.
ACCESSION M34024
VERSION M34024.1 GI:185267
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain; processed
gene.
SOURCE Homo sapiens (individual isolate H8409) (clone: M43) 104 day foetus
liver cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 470)
AUTHORS Schroeder,H.W. Jr. and Wang,J.Y.
TITLE Preferential utilization of conserved immunoglobulin heavy chain
variable gene segments during human fetal life
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 872 (1691), 6146-6150 (1990)
MEDLINE 90349571
COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad.
Sci. U.S.A. (1990) in press] kindly submitted
by H.W.Schroeder,Jr., 04-MAY-1990.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="liver"
/dev_stage="104 day foetus"
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<1..>470
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/protein_id="AAA69729.1"
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/db_xref="GDB:G00-118-731"
/translation="GIFRCPHLVIRTEORELTMEFGLSWLFLVAILKGVOCEVOLLES
GGGLVOPGGSRLSCASGTFSSYAMSVROAPGKLEWVSALSGSGSTYYADSVK
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404..405
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/organism="Homo sapiens"
422..423
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BASE COUNT 101 a 110 c 146 g 113 t
ORIGIN
Query Match 67.4%; Score 277.2; DB 9; Length 470;
Best Local Similarity 82.6%; Pred. No. 2.1e-64;
Matches 347; Conservative 0; Mismatches 58; Indels 15; Gaps 2;
QY 1 ATGAGTTTGGCTGAGCTGGGTTTCTCTCTCTTTTGAAGGTGTCAGGTGAG 60
DB 57 ATGAGTTTGGCTGAGCTGGGTTTCTCTCTCTTTTGAAGGTGTCAGGTGAG 116
QY 61 GTGCAGCTGCTGGAGTCTGGGCGGCTTGCAGGAGCTGGGGGTCCCTGAGACTCTCC 120
DB 117 GTGCAGCTGCTGGAGTCTGGGCGGCTTGCAGGAGCTGGGGGTCCCTGAGACTCTCC 176

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BASE COUNT		93 a	104 c	136 g	104 t
ORIGIN					
Query Match		67.4%; Score 277; DB 9; Length 437;			
Best Local Similarity		83.2%; Pred. No. 2.4e-64;			
Matches 342; Conservative		0; Mismatches 60; Indels 9; Gaps 2;			
Qy	1	ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTTGTTCTCTTTTCAAAGGTGTCAGTGTGAG	60		
Db	36	ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTTGTTCTCTTTTAAAGGTGTCAGTGTGAG	95		
Qy	61	GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC	120		
Db	96	GTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTACATCCTGGGGGTCCCTGAGACTCTCC	155		
Qy	121	TGCGCAGCCTCCGGGTTCAAGTTCACTTCAATAACTACTACATGGACTGGGTCCGCCAG	180		
Db	156	TGTGCAGCCTCTG-----GATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAG	209		
Qy	181	GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGATCCCAACATGG	240		
Db	210	GCTCCAGGGAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTAGCACATAC	269		
Qy	241	TACGCACTCCGTGAAGGGCAGATTCAACATCTCCAGAGAGAACGCCAACACACTG	300		
Db	270	TACTCAGACTCCGTGAAGGGCCGGCTCACCATCTCCAGAGACAATTCGAAGAACACGCTG	329		
Qy	301	TTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG	360		
Db	330	TATCTGCAAAATGAACAGCCTGAGAGCCGAGACACGGCCGTATATTACTGTGCCAGATGG	389		
Qy	361	ACTACAGGGTCTGACTCTCCTGGGGCCAGGGAGTCTCTGGTCACCGTCTCCTCA	411		
Db	390	---CGGATCTAGACTACTTGGGGCCAGGGAACCTGGTCACCGTCTCCTCA	437		

Search completed: July 15, 2003, 10:00:31
Job time : 1380.91 secs


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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3054342"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B [UT1]"
/notes="Vector: pTT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldio, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      89 a   93 c   123 g   100 t
ORIGIN

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Query Match      69.9%; Score 287.2; DB 10; Length 406;
Best Local Similarity 83.0%; Pred. No. 5.7e-70;
Matches 341; Conservative 0; Mismatches 64; Indels 6; Gaps 1;

Qy 1 ATGGAGTTTGGCTGAGCTGGGTTTCTCTGTTCTTTGAAAGGTGTCAGTGTGAG 60
Db 2 ACCAGTTGGGCTGTGCTGGGTTTCTTTGTTGTTATTTAGAAAGGTGTCAGTGTGAG 61

Qy 61 GTGCAGCTGGTGTGAGTCTGGGGGGCTTGGCAAGCCTGGGGGTCCTCGAGACTCTCC 120
Db 62 GTGCAGCTGGTGTGAGTCTGGGGGGCTTGGTACAGCCTGGAGGTCCTCGAGACTCTCC 121

Qy 121 TCCGAGCTCCGGTTGAGTTTCACTTCACTTAATACTACTAGTGGTGGTCCGCCAG 180
Db 122 TGTGAGCCTCTG-----GATTCACCTTCAGTAGTTATGAATGAATGAGTGGTCCGCCAG 175

Qy 181 GCTCAGGCGAGGGCTGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCCACTGG 240
Db 176 GCTCAGGGAAGGGCTGAGTGGGTTCATACATTAGTAGTGGTGTATCCATATAC 235

Qy 241 TACGAGACTCCGTGAAGGGCAGATTACCAATCTCCAGAGAACCCCAACAACACTG 300
Db 236 TACGAGACTCTGTGAAGGGCGATTACCAATCTCCAGAGAACCCCAACAACACTG 295

Qy 301 TTCTTCAATGAACAGCTGAGCTGAGGACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 296 TATCTGCAATGAACAGCTGAGGACGGCTGTCTATTACTGTGCGAGTCAA 355

Qy 361 ACTCAGGCTGTGACTCTCTGGGGCCAGGAGTCTGCTCAGCTCTCTCTCA 411
Db 356 TATAACAACAGCTGTGACTGGGGCCAGGAGTCTGCTCAGCTCTCTCTCA 406

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RESULT 2
BM007475      613 bp  mRNA  linear  EST 30-OCT-2001
LOCUS         60361742F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5440475 5',
DEFINITION    mRNA sequence.
ACCESSION     BM007475
VERSION       BM007475.1 GI:16521829
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 613)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              cDNA Library preparation: Ling Hong/Rubin Laboratory
              Tissue Procurement: Dr. Mark Watson
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.llnl.gov
Plate: L1CM1913 row: d column: 12
High quality sequence stop: 608.
Location/Qualifiers
Source
1..613
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5440475"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
BASE COUNT    126 a   172 c   174 g   141 t
ORIGIN

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Query Match      68.5%; Score 281.6; DB 13; Length 613;
Best Local Similarity 83.6%; Pred. No. 2.4e-68;
Matches 346; Conservative 0; Mismatches 59; Indels 9; Gaps 2;

Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTGTTCTTTGAAAGGTGTCAGTGTGAG 60
Db 64 ATGGAACCTGGGGCTCCGCTGGGTTTCTTTGTTGTTATTTAGAAAGGTGTCAGTGTGAG 123

Qy 61 GTGCAGCTGGTGTGAGTCTGGGGGGCTTGGCAAGCCTGGGGGTCCTCGAGACTCTCC 120
Db 124 GTGCAGCTGGTGTGAGTCTGGGGGGCTTGGTCAAGCCTGGGGGTCCTCGAGACTCTCC 183

Qy 121 TGCGACGCTCCGGTTTCAGGTTTCACTTCAATAACTACTACATGAGTGGTCCGCCAG 180
Db 184 TGTGACGCTCTG-----GAATCACCTTCAGTAACCTATACGTGAACCTGGTCCGCCAG 237

Qy 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCCACTGG 240
Db 238 GCTCCAGGAAGGGCTGGAGTGGGTCTCATCCATTAGTAGTGTAGTATACATATAC 297

Qy 241 TACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAACCCCAACAACACTG 300
Db 298 TACGAGACTCAGTGAAGGGCCGATTACCATCTCCAGAGAACCCCAACAACACTG 357

Qy 301 TTCTTCAATGAACAGCTGAGAGCTGAGACAGCTGTCTATTACTGTGCGAG---C 357
Db 358 TGGCTGCAATGAACAGCTGAGAGCCGCTGAGAGCCGAGTGTCTATTACTGTGCGAGGCC 417

Qy 358 TTGACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTGCTCAGCTCTCTCTCA 411
Db 418 CAGGCTGTTTCTTCGACTACTGGGGCCAGGAGCCCTGGTCCCGTCTCTCTCA 471

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RESULT 3
AW402613      511 bp  mRNA  linear  EST 16-FEB-2000
LOCUS         UI-HF-BKO-aax-g-05-0-UI_r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION    IMAGE:3055305 5', mRNA sequence.
ACCESSION     AW402613
VERSION       AW402613.1 GI:6921317
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 511)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Eco RI site shown at the beginning of the sequence.

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DEFINITION  UI-HF-BKO-aag-a-05-0-UI-r1 NIH MGC 36 Homo sapiens cDNA clone
IMAGE:3054608 5', mRNA sequence.
ACCESSION    AW402793
VERSION      AW402793.1  GI:6921535
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      1 (bases 1 to 447)
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              cDNA Library Arrayed by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.
              Location/Qualifiers
FEATURES     source
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:3054608"
                /clone_lib="NIH MGC_36"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_host="DH10B (LTI)"
                /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   97 a 110 c 137 g 103 t
ORIGIN
1 ATGGAGTTGGCTGAGCTGGGTTTCTTCTTCTTTGAAAGGTGTCAGTGTGAG 60
2 ATGGAAGTGGGCTCCGCTGGGTTTCTTCTTCTTTTGAAGGTGTCAGTGTGAG 97
3 ATGCAAGTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 120
4 GTGCAGCTGGTGGGTTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 157
5 TGTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 180
6 TGTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 211
7 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 240
8 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 271
9 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 300
10 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 331
11 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 360
12 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 391
13 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 411
14 GTTCAGAGCTCTGGATTACAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 442
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RESULT 6
LOCUS      AW403220
DEFINITION  UI-HF-BKO-aay-h-04-0-UI-r1 NIH MGC 36 Homo sapiens cDNA clone
IMAGE:3055710 5', mRNA sequence.
ACCESSION  AW403220
VERSION     AW403220.1  GI:6922096
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS      1 (bases 1 to 471)
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Eco RI site shown at the beginning of the sequence.
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: M.B. Soares Lab
              cDNA Library Arrayed by: M.B. Soares Lab
              DNA Sequencing by: M.B. Soares Lab
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward.
              Location/Qualifiers
FEATURES     source
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
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                /clone_lib="NIH MGC_36"
                /tissue_type="lymph"
                /cell_type="germinal center B cells"
                /cell_line="MGC85"
                /lab_host="DH10B (LTI)"
                /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
                Constructed from size fractionated cytoplasmic mRNA
                (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                M. Staudt, Ph.D. Library preparation by Maria de Fatima
                Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT   98 a 127 c 143 g 103 t
ORIGIN
1 ATGGAGTTGGCTGAGCTGGGTTTCTTCTTCTTTTGAAGGTGTCAGTGTGAG 60
2 ATGGAAGTGGGCTCCGCTGGGTTTCTTCTTCTTTTGAAGGTGTCAGTGTGAG 78
3 GTGCAGCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 120
4 GTGCAGCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 138
5 TGCGAGAGCTCTGGGTTTCAAGTTTCACTTCAATAAATCTACATGAGACTGGTCCGCCAG 180
6 TGTCAGAGCTCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 192
7 GTTCAGAGCTCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 240
8 GTTCAGAGCTCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 252
9 GTTCAGAGCTCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 300
10 GTTCAGAGCTCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 312
11 GTTCAGAGCTCTGGTGGAGTCTGGGGAGGCTGGTCAAGCTGGGGGTCTCTGAGACTCTCC 354
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QY 121 TCGCAGCCTCCGGGTTCCAGTTCCATTCAATAACTACTACATGAGACTGGTCCGCCAG 180
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 Db 173 TGTGAGCCTCTG-----GATTACCTTTAGCAGCTGTGGCATGAGCTGGGTCCGCCAG 226
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 QY 181 GCTCAGGCGAGGGCTGAGTGGGTCTCACGTAATTAGTAGTGGTGTATCCCATG 240
 |||||
 Db 227 GCTCCAGGAAGGGCTGAGTGGGTCTCAAGTATTAGTGGTAAATGGTGTAGCACATAC 286
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 QY 241 TACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAACGCCAACACACACTG 300
 |||||
 Db 287 TACGAGACTCCGTGAAGGCGGGTTCCATCTCCAGAGACAAATCCAAAGAACAGCTG 346
 |||||
 QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGGTCTTATTACTGTGCGA----- 355
 |||||
 Db 347 TATCTGCAATGAACAGCCTGAGAGCGGAGGACAGCGCGTATATTTCTGTGCGAAGGT 406
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 QY 356 -----GCTTCACTACAGGCTCTGACTCTCCGGGCGAGGAGTCTCGTCACTCTCC 408
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 Db 407 CAGCCCTTCTGACTAACTTCTGACTACTGGGCGCAGGGAACGCTGTCACCGTCTCC 466
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 QY 409 TCA 411
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 Db 467 TCA 469

RESULT 9
 AW403059
 LOCUS
 DEFINITION UI-HF-BK0-aai-f-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3054090 5', mRNA sequence.

ACCESSION
 AW403059
 VERSION
 AW403059.1 GI:6921885

KEYWORDS
 EST.

SOURCE
 human.

ORGANISM
 Homo sapiens

REFERENCE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
 1 (bases 1 to 456)

TITLE
 NIH-MGC http://mgi.nci.nih.gov/

JOURNAL
 National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward

Location/Qualifiers

1. .456

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3054090"

/clone_lib="NIH_MGC_36"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/note="Vector: pTT3-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(0.5-1.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

103 a 104 c 139 g 110 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 66.2%; Score 272.2; DB 10; Length 456;

Matches 320; Conservative 84.4%; Pred. No. 9.6e-66;

Mismatches 53; Indels 6; Gaps 1;

QY 1 ATGAGTTTGGGCTGAGCTGGGTTTCTCTGTTCTCTTTGAAAGGTGTCCAGTGTGAG 60
 |||||
 Db 52 ATGAGTTTGGGCTGCTGCTGGGTTTCTCTGTTCTCTTTAGAAAGGTGTCCAGTGTGAG 111
 |||||
 QY 61 GTGAGCTGTGTGGAGTCTGGGGCGGCTTGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
 |||||
 Db 112 GTGAGCTGTGTGGAGTCTGGGGGAGGCTTGATACAGCCTGGAGGTCCTGAGACTCTCC 171
 |||||
 QY 121 TGCCAGCCTCCGGTTCAGGTTCCACCTTCAATTAATCTACTACATGGAGTGGTCCGCCAG 180
 |||||
 Db 172 TGTGACGCTCTG-----GATTACACCTTCAGTAGTTATGGAATGAATGGGTCCGCCAG 225
 |||||
 QY 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGTGATGCCACATGG 240
 |||||
 Db 226 GCTCAGGGAAGGGCTGGAGTGGGTTTATACATTAGTAGTGTGATGACATATAC 285
 |||||
 QY 241 TACGAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCAACACACTG 300
 |||||
 Db 286 TACGAGACTCTGTGAAGGCGCGATTCCACCATCTCCAGAGACAAACGCAACTCACTG 345
 |||||
 QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGAGCAGGCTGTCTATTACTGTGCGAGCTTG 360
 |||||
 Db 346 TATCTGCAATGAAGAGCCTGAGAGCGGAGGACACGCGCTGTTATTACTGTGCGAGCCAT 405
 |||||
 QY 361 ACTACAGGCTCTGACTCCT 379
 |||||
 Db 406 ATACAGCAGCTGACGACT 424

RESULT 10

AW401386

LOCUS

DEFINITION

UI-HF-BK0-aau-h-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone

IMAGE:3055324 5', mRNA sequence.

ACCESSION

AW401386

VERSION

AW401386.1 GI:6920168

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 582)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward

Location/Qualifiers

1. .582

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3055324"

/clone_lib="NIH_MGC_36"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/note="Vector: pTT3-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(0.5-1.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

117 a 155 c 169 g 141 t

BASE COUNT

/note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldio, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 93 a 116 c 131 g 103 t

ORIGIN

Query Match 65.9%; Score 271; DB 10; Length 443;
Best Local Similarity 81.6%; Pred. No. 2.1e-65;
Matches 345; Conservative 0; Mismatches 60; Indels 18; Gaps 2;

Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTTCCTTTTGAAGGTGTCAGTGTGAG 60
Db 25 ATGGAACCTGGGCTCGCTGGGTTTCTTGTTCCTTTTGAAGGTGTCAGTGTGAG 84

Qy 61 GTGCAGCTGTGAGTCTGGGGGGCTTGGCAAGCCTGGGGGTCTCTGAGACTCTCC 120
Db 85 GTGCAGCTGTGAGTCTGGGGGGCTTGGCAAGCCTGGGGGTCTCTGAGACTCTCC 144

Qy 121 TCGCAGCCTCCGGGTTACGTTTCACTTCAATACTACTACAGCTGGGTCCGCCAG 180
Db 145 TGTGAGCCTCTG-----GATTACCTTCACTACTATACAGCTGGGTCCGCCAG 198

Qy 181 GTCCAGGGCAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGAATCCCATGG 240
Db 199 GTCCAGGGAAGGGCTGGAGTGGGTCTCATTCCATGAGTAGTGGTACTTACATATAC 258

Qy 241 TACGAGACTCGTGAAGGGAGATTACCATCTTCAGAGAGAAAGCCAAACACACTG 300
Db 259 TACGAGACTCAGTGAAGGGCGATTACCATCTTCAGAGAGAAAGCCAAACACTG 318

Qy 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAGCTG 360
Db 319 TATCTGCAGATGAACAGCTGAGAGCGGAGGACACCGCTGTCTATTACTGTGCGAGAGA 378

Qy 361 ACTACAGGG-----TCTGACTCTCGGGCCAGGGAGTCTGTGTACCGCTCTCC 408
Db 379 GTTCCATGTTTCAGTTCTACTTTGACTACTGGGCCAGGGAACCTGTGTACCGCTCTCC 438

Qy 409 TCA 411
Db 439 TCA 441

RESULT 13
AW408304
LOCUS
DEFINITION
UI-HF-BK0-abj-e-10-0-UI.r1 NIH MGC 36 Homo sapiens cDNA clone
IMAGE:3056371 5', mRNA sequence.

ACCESSION
AW408304
VERSION
AW408304.1 GI:6927361
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 440)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab.
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers

1. .440
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056371"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_hosts="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldio, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 99 a 98 c 134 g 109 t

ORIGIN

Query Match 65.7%; Score 270; DB 10; Length 440;
Best Local Similarity 87.1%; Pred. No. 3.9e-65;
Matches 310; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

Qy 1 ATGAGATTGGGCTGAGCTGGGTTTCTTGTTCCTTTTGAAGGTGTCAGTGTGAG 60
Db 62 ATGAGATTGGGCTGCTGGGTTTCTTGTTCCTTTTGAAGGTGTCAGTGTGAG 121

Qy 61 GTGCAGCTGTGAGTCTGGGGGGCTTGGCAAGCCTGGGGGTCTCTGAGACTCTCC 120
Db 122 GTGCAGCTGTGAGTCTGGGGGGCTTGGTACAGCTGGAGGTCTCTGAGACTCTCC 181

Qy 121 TGCAGAGCTCCGGGTTCAAGTTCACTTCAATTAACACTACATGGAGTGGGTCCGCCAG 180
Db 182 TGTGAGCCTCTG-----GATTACCTTCACTAGTATTATGAATGAACCTGGGTCCGCCAG 235

Qy 181 GCTCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATGCCACATGG 240
Db 236 GCTCAGGGAGGGGGCTGGAGTGGGTTTTCATACATTAGTAGTGGTAGTACCATATAC 295

Qy 241 TACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAAAGCCAAACACACTG 300
Db 296 TACGAGACTCTGTGAAGGGCCGATTACCATCTCCAGAGAGAAAGCCAAACACTG 355

Qy 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAG 356
Db 356 TATCTGAAATGAACAGCTGAGAGCGGAGGACAGCGTGTCTATTACTGTGCGAG 411

RESULT 14
AW403862
LOCUS
DEFINITION
UI-HF-BK0-abo-a-12-0-UI.r1 NIH MGC 36 Homo sapiens cDNA clone
IMAGE:3056926 5', mRNA sequence.

ACCESSION
AW403862
VERSION
AW403862.1 GI:6923015
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 487)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.


```
FT      misc_feature      /note= "encodes CDR 2 region"
FT      358..378
FT      /*tag= f
FT      /note= "encodes CDR 2 region"
XX
PN      WO9837099-A1.
XX
PD      27-AUG-1998.
XX
XX      17-FEB-1998; 98WO-US02253.
XX
PR      05-FEB-1998; 98US-0803085.
PR      20-FEB-1997; 97US-0803085.
XX
PA      (IDEC-) IDEC PHARM CORP.
PA      (SEK) SEIKAGAKU CORP.
XX
PI      Klotzer WS, Nakamura T, Reff ME;
XX
DR      WPI; 1998-467495/40.
DR      P-PSDB; AAW70380.
XX
XX      New anti-human CD23 monoclonal antibody - used for inhibiting IgE
PT      expression to treat or prevent allergic, inflammatory and
PT      auto:immune conditions
XX
PS      Example 1; Pages 108-110; 146pp; English.
XX
CC      The present sequence represents a DNA sequence encoding the heavy
CC      chain variable region of primate monoclonal antibody anti-human CD23 SE8.
CC      The invention provides primate monoclonal antibodies which specifically
CC      bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
CC      and comprise either of a human gamma-1 or human gamma-3 constant region
CC      that binds to human Fc gamma receptors and inhibits IgE expression.
CC      The monoclonal antibodies of the invention are claimed to be useful
CC      for inhibiting induced IgE production for treating or preventing
CC      allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
CC      conjunctivitis, autoimmune haemolytic anaemia, etc.
XX
SQ      Sequence 411 BP; 80 A; 102 C; 130 G; 99 T; 0 other;

Query Match      99.2%; Score 407.8; DB 19; Length 411;
Best Local Similarity 99.5%; Pred. No. 4.8e-105;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGAGTTTGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAGGTTCCAGTGTGAG 60
Db      |||
QY      1  ATGGAGTTTGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAGGTTCCAGTGTGAG 60
Db      |||
QY      61  GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTTGGGGGTCCCTGAGACTCTCC 120
Db      |||
QY      61  GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTTGGGGGTCCCTGAGACTCTGG 120
Db      |||
QY      121  TCGCAGCCTCCGGGTTTCAAGTTTCACTTCAATACTACTATGAGACTGGGTCCGCCAG 180
Db      |||
QY      121  TCGCAGCCTCCGGGTTTCAAGTTTCACTTCAATACTACTATGAGACTGGGTCCGCCAG 180
Db      |||
QY      181  GCTCCAGGCGAGGGCTGAGTGGGTCTCACCTATTAGTAGTGGTATCCCAATGG 240
Db      |||
QY      181  GCTCCAGGCGAGGGCTGAGTGGGTCTCACCTATTAGTAGTGGTATCCCAATGG 240
Db      |||
QY      241  TACGCAGACTCCGTGAAGGCGAGATTCACTCTCCAGAGAGAACGCCAACACACTG 300
Db      |||
QY      241  TACGCAGACTCCGTGAAGGCGAGATTCACTCTCCAGAGAGAACGCCAACACACTG 300
Db      |||
QY      301  TTTCCTCAATGAACAGCCTGAGAGCTGAGGACAGGCTGTATTACTGTGCGAGCTTG 360
Db      |||
QY      301  TTTCCTCAATGAACAGCCTGAGAGCTGAGGACAGGCTGTATTACTGTGCGAGCTTG 360
Db      |||
QY      361  ACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGGTCCACCGTCTCTCA 411
Db      |||
QY      361  ACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGGTCCACCGTCTCTCA 411
Db      |||
```

```
RESULT 2
AAV61794
ID      AAV61794 standard; DNA; 19035 BP.
XX
AC      AAV61794;
XX
DT      07-JUN-1999 (first entry)
XX
DE      Traget plasmid Mandy containing anti-CD23 gene.
XX
XX      Mandy; target plasmid; gene integration; gene amplification;
KW      homologous recombination; vector; neomycin phosphotransferase;
KW      neo gene; selectable marker; immunoglobulin; CD23; SE8; human; ss.
XX
OS      Chimeric - Mus sp.
OS      Chimeric - Escherichia coli.
OS      Chimeric - Baculovirus.
OS      Chimeric - Cytomegalovirus.
OS      Chimeric - Rhesus macaque polyoma virus.
OS      Chimeric - Photinus sp.
OS      Chimeric - Salmonella typhimurium.
OS      Chimeric - Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      misc_feature 361
FT      /*tag= a
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc_feature 721
FT      /*tag= b
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc_feature 2941
FT      /*tag= c
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc_feature 3301
FT      /*tag= d
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc_feature 4261
FT      /*tag= e
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc_feature 4621..4622
FT      /*tag= f
FT      /note= "these bases represent nucleotides missing
FT      from the sequence given in the
FT      specification. They are included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc_feature 8161
FT      /*tag= g
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
```



```
QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGGTGCTATTACTGTGCGAGCTTG 360-
Db 9732 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGGTGCTATTACTGTGCGAGCTTG 9791
QY 361 ACTACAGGCTGCTGACTCTCTGGGGCCAGGAGTCTGGTCCACCGTCTCTCTCA 411
Db 9792 ACTACAGGCTGCTGACTCTCTGGGGCCAGGAGTCTGGTCCACCGTCTCTCTCA 9842

RESULT 3
AAH41153
ID AAH41153 standard; DNA; 458 BP.
XX
AC AAH41153;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human coding sequence SEQ ID 3.
XX
KW Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;
KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;
KW signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
XX
OS Homo sapiens.
XX
PN WO200136642-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-JP08129.
XX
PR 18-NOV-1999; 99JP-0328681.
XX
PR 08-NOV-2000; 2000JP-0340216.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
PI Sakamoto S, Kamada M;
XX
WPI; 2001-343825/36.
XX
P-PSDB; AAB99111.
XX
Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT useful for treating TGF-beta associated diseases such as tissue
PT fibrosis.
XX
PS Example 12; Page 94-95; 118pp; Japanese.
XX
CC The present invention relates to novel human monoclonal antibodies. The
CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC receptor, resulting in the inhibition of the signal transduction of human
CC TGF-beta into cells. The antibodies can be used for the prevention and
CC treatment of diseases associated with the production of TGF-beta, such as
CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,
CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
CC used in the present invention.
XX
SQ Sequence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;

Query Match 72.1%; Score 296.2; DB 22; Length 458;
Best Local Similarity 84.4%; Pred. No. 1.3e-73;
Matches 347; Conservative 0; Mismatches 58; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGCTTTCTTGTTCTCTTTTGAAGGTTCTCAGTGTCGAG 60
Db 1 ATGGAACTGGGGCTCGCTGGGTTTCTTGTTGCTATTATTAAGAGGTTCTCAGTGTCGAG 60
QY 61 GTGCAGCTGGTGGAGTCTCGGGGCGGCTTTGGCAAGCCTTGGGGGTCTCCTGAGACTCTCC 120
Db 61 GTGCAGCTGGTGGAGTCTCGGGGAGGCGCTGGTCAAGCCTTGGGGGTCTCCTGAGACTCTCC 120
QY 121 TCGCAGCCTCGGGTTACGTTTACCTTCAATACTACTACATGACTGGGTCCGCCAG 180
Db 121 TGTGAGCGCTCTG-----GATTTCACCTTCAGTAGCTTTAGCATGAAGTGGGTCCGCCAG 174
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QY 181 GCTCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGATCCACATGG 240
Db 175 GCTCAGGAAGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTATATATAC 234
QY 241 TACCAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAAACGCCAACACACTG 300
Db 235 TACACAGACTCAGTGAAGGGCCGATTACCATCTCCAGAGACAACGCCCAAGAACTCACTG 294
QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGGTGCTATTACTGTGCGAGCTTG 360
Db 295 TATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGG 354
QY 361 ACTACAGGCTGCTGACTCTCTGGGGCCAGGAGTCTGGTCAACCGTCTCTCTCA 411
Db 355 TACTGGGGTTTGACTACTAGGGCCAGGGAACCTGGTCAACCGTCTCTCTCA 405

RESULT 4
AAS22533
ID AAS22533 standard; cDNA; 1710 BP.
XX
AC AAS22533;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human cDNA encoding a novel human protein #99.
XX
KW Human; novel protein; ss; Antianemic; osteopathic; antiinflammatory;
KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
OS Homo sapiens.
XX
PN WO200155437-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02623.
XX
PR 25-JAN-2000; 2000US-0491404.
XX
PA (HYSE-) HYSEQ INC.
XX
Tang YT, Liu C, Drmanac RT;
WPI; 2001-451939/48.
P-PSDB; AAU14228.
Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage.
XX
PS Claim 1; Page 306-308; 894pp; English.
XX
CC The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicit an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet
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RESULT 6
AAV24243
ID AAV24243 standard; cDNA to mRNA; 411 BP.
XX
AC AAV24243;
XX
DT 03-SEP-1998 (first entry)
XX
DE Chimeric antibody fragment against hTPRP encoding cDNA SEQ ID NO:58.
XX
KW Chimeric; antibody; human parathormone related peptide; hTPRP; mouse;
KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;
KW hypophosphemia; pathogen; vitamin D resistance; V region; C region;
KW humanised; ds.
XX
XX Synthetic.
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..411
FT /*tag= a
FT /note= "no stop codon given"
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..411
FT /*tag= c
XX
PN WO9813388-A1.
XX
XX 02-APR-1998.
XX
XX 24-SEP-1997; 97WO-JP03382.
XX
XX 24-JUL-1997; 97JP-0214168.
XX
XX 26-SEP-1996; 96JP-0255196.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Sato K, Wakahara Y, Yabuta N;
XX
XX WPI; 1998-230640/20.
XX
XX P-PSDB; AAW57603.
XX
XX New chimeric antibodies against human parathormone related
XX peptide(s) - useful for, e.g. treatment of hypercalcaemia and other
XX disorders caused by malignant neoplasm(s)
XX
XX Claim 60; Page 122-123; 182pp; Japanese.
XX
XX New antibodies have been developed which are specific for human
XX parathormone related peptides (hTPRP). The antibodies comprise chimeric
XX L and/or H chains, where the C region is of human and L region of mouse,
XX origin. The present sequence encodes a specifically claimed region of
XX an antibody of the invention. Host cells, transformed with vectors
XX containing DNA encoding antibodies of the invention, can be used to
XX produce the antibodies. The antibodies may be used to treat
XX hypercalcaemia, especially that due to a malignancy, e.g. cancers of
XX pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
XX breast, kidney, bladder, womb or prostate or malignant lymphoma. They
XX may also be used for treatment of hypophosphemia such as that due to
XX pathogens or to vitamin D resistance.
XX
XX Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
XX
Query Match 65.8%; Score 270.6; DB 19; Length 411;
Best Local Similarity 81.8%; Pred. No. 2e-66;
Matches 341; Conservative 0; Mismatches 64; Indels 12; Gaps 2;
XX
XX 1 ATGGAGTTGGCTGAGCTGGGTTTCTTGTCTTTTGAAGAGTGTCAGTGTGAG 60
XX |||||
XX 1 ATGGGGTTGGCTGAGCTGGGTTTCTTGTCTTTTGAAGAGTGTCAGTGTGAG 60

```

```

61 GTGCAGCTGGTGGAGTCTGGGGGCGGCTTGCAAGCCTGGGGGCTCCCTGAGACTCTCC 120
|||||
61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120
|||||
121 TGCGACGCTCCGGTTTCAGGTTCACTTCAATTAATCTACTACATGGAGTGGGTCCGCCAG 180
|||||
121 TGTGACGCTCTG-----GATTCACTTCAGTAGCTATGGCATGTCTTGGGTCCGCCAG 174
|||||
181 GCTCCAGGCGAGGGCTGGAGTGGTCTCAGTATTTAGTAGTAGTGTGATCCACATGG 240
|||||
175 GCTCCAGGCGAAGGGCTGGAGTGGTGGCAACCAATTAGTAGTGTGTAGTTACACCTAC 234
|||||
241 TACGACAGCTCCGTTGAAGGCGAGATTCAACCATCTCCAGAGAGAACGCCAACACACTG 300
|||||
235 TATCCAGACAGTGTGAAGGGCGGATTCACTATCTCCAGAGACAAATTCAGAACACGCTG 294
|||||
301 TTTCTTCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGTTG 360
|||||
295 TATCTGCAAAATGAACAGCCTTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGACAG 354
|||||
361 ACTACAGGCTCTGAC-----TCTGGGGCGCAGGAGTCTCTGTCACGGTCTCTCTCA 411
|||||
355 ACTACTATGACTTACTTTTGTCTTACTTGGGGCGCAGGGAACCTGTGTCACCGTCTCTCTCA 411
|||||

RESULT 7
AAAX00116
ID AAX00116 standard; cDNA to mRNA; 411 BP.
XX
XX AC AAX00116;
XX
XX 14-APR-1999 (first entry)
XX
XX Human antibody heavy chain coding sequence.
XX
XX Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
XX inhibitor; humanised; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
CDS 1..411
FT /*tag= a
FT /note= "no stop codon given"
XX
XX WO9851329-A1.
XX
XX 19-NOV-1998.
XX
XX 13-MAY-1998; 98WO-JP021116.
XX
XX 18-JUL-1997; 97JP-0194445.
XX
XX 15-MAY-1997; 97JP-0125505.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Ishii K, Sato K, Tunenari T;
XX
XX WPI; 1999-070101/06.
XX
XX P-PSDB; AAW89635.
XX
XX Inhibitors of binding of parathyroid hormone related peptide to its
XX receptor - useful for, e.g. treatment of cachexia arising from
XX cancer or other diseases
XX
XX Example 4; Page 83-84; 125pp; Japanese.
XX
XX The present invention describes compositions for the treatment of
XX cachexia containing a substance which inhibits the binding of a
XX parathyroid hormone related peptide (PTHrP) to its receptor, as an
XX active component. This substance may be an antagonist to the receptor,
XX or an antibody (preferably monoclonal) or antibody fragment,

```


CC vomiting, diarrhoea, fever, perspiration and diabetes. AAF69085 to
CC AAF69140 and AAB76897 to AAB76897 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;

Query Match 65.8%; Score 270.6; DB 22; Length 411;
Best Local Similarity 81.8%; Pred. No. 2e-66;
Matches 341; Conservative 0; Mismatches 64; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60
Db 1 ATGGGTTTGGGCTGAGCTGGGTTTCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60

QY 61 GTGCAGCTGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 120
Db 61 GTGCAGCTGGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 120

QY 121 TCGCAGCTCCGGGTTTCAGGTTCACTTCAATAACTACTATGAGCTGGGTCGCGCAG 180
Db 121 TGTGAGCTCTG-----GATTCACCTTCAGTAGCTATGGCATGTCTTGGGTCCGCCAG 174

QY 181 GCTCAGGCGAGGCTGAGTGGGTCTCAGTATAGTAGTGGTATCCCACTGG 240
Db 175 GCTCAGGCGAAGGCTGAGTGGGTCTCAGTATAGTAGTGGTATCCCACTGG 234

QY 241 TATCCAGAGCTCGTGAAGGCGAGATTCCATCTCCAGAGAACCGCAACACACTG 300
Db 235 TATCCAGAGCTCGTGAAGGCGAGATTCCATCTCCAGAGAACCGCAACACACTG 294

QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGCTTG 360
Db 295 TATCTGCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGACAG 354

QY 361 ACTCAGGCTGTGAC-----TCCTGGGCGCAGGAGTCTCGTCACTCTCTCA 411
Db 355 ACTACTATGACTTACTTTGCTTACTTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 411

RESULT 13
ID AAF69186 standard; DNA; 411 BP.
XX AAF69186;
DT 17-APR-2001 (first entry)
XX Human antibody H chain protein SEQ ID NO:58.
DE Human; mouse; hypercalcaemia; parathyroid hormone; PTH; PTHrP;
KW parathyroid hormone related peptide; analgesic; immunosuppressive;
KW neurotropic; neuroprotective; antiinflammatory; cyostatic; antithyroid;
KW eating-disorder; cardiovascular; pain; immune suppression; appetite;
KW digestive system; protein metabolism; sugar metabolism; lipid metabolism;
KW blood chemistry; thyroid function; electrolyte balance; neurological;
KW central nervous system disorder; sleep disturbance; brain function;
KW brain circulation; autonomic nervous system; blood poisoning; dropsy;
KW inflammation; blood disease; calcium disturbance; autoimmune disease; ds.
XX Homo sapiens.
OS
XX
XX WO200102011-A1.
PN
PD 11-JAN-2001.
XX
PF 03-JUL-2000; 2000WO-JP04414.
XX
PR 02-JUL-1999; 99JP-0189793.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Ogata E, Sato K, Onuma E, Teunenari T, Saito H, Azuma Y;
XX

DR WPI; 2001-123065/13.
XX Agents modifying the binding of ligands to parathyroid hormone receptor
PT or parathyroid hormone related peptide receptor for treatment of
PT disorders associated with parathyroid hormone other than hypercalcaemia
PT
XX Example; Page 101-102; 130pp; Japanese.

CC The present invention describes an agent (I) for the treatment and
CC prevention of diseases other than hypercalcaemia associated with
CC parathyroid hormone (PTH) or parathyroid hormone related peptide (PTHrP).
CC (I) contains an active component a substance which promotes or
CC inhibits the binding of ligands to PTH receptor or PTHrP receptor, or is
CC an agonist or antagonist to these receptors. (I) have analgesic,
CC immunosuppressive, neurotropic, neuroprotective, antiinflammatory,
CC cyostatic, antithyroid, eating-disorders and cardiovascular activities.
CC (I) is used for treatment and prevention of disorders associated with PTH
CC or PTHrP, including: pain; immune suppression; disturbances of the
CC digestive system; protein metabolism; sugar metabolism; lipid metabolism;
CC appetite, blood chemistry, thyroid function, and electrolyte balance;
CC central nervous system disorders such as sleep disturbance, neurological
CC disturbances, brain function disturbance, brain circulation disturbance
CC and autonomic nervous system disturbance; and disorders caused by PTH or
CC PTHrP associated cytokine cascade including blood poisoning, dropsy,
CC inflammation, blood disease, calcium disturbance and autoimmune disease.
CC Treatment and prevention of disorders other than hypercalcaemia which
CC are associated with PTH or PTHrP, especially those associated with
CC malignant tumours, and thereby ameliorating the quality of life of these
CC patients. AAF69141 to AAF69196 and AAB76898 to AAB76916 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;

Query Match 65.8%; Score 270.6; DB 22; Length 411;
Best Local Similarity 81.8%; Pred. No. 2e-66;
Matches 341; Conservative 0; Mismatches 64; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60
Db 1 ATGGGTTTGGGCTGAGCTGGGTTTCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60

QY 61 GTGCAGCTGGTGGGCTGGGCGGCTTGGCAAGCCTTGGGGGTCCTCGAGACTCTCC 120
Db 61 GTGCAGCTGGTGGGCTGGGCGGCTTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120

QY 121 TGCAGGCTCCGGGTTTCAGGTTTCACTTCAATAACTACTATGAGCTGGGTCGCGCAG 180
Db 121 TGTGAGCTCTG-----GATTCACCTTCAGTAGCTATGGCATGTCTTGGGTCCGCCAG 174

QY 181 GCTCAGGCGAAGGCTGAGTGGGTCTCAGTATAGTAGTGGTATCCCACTGG 240
Db 175 GCTCAGGCGAAGGCTGAGTGGGTCTCAGTATAGTAGTGGTATCCCACTGG 234

QY 241 TATCCAGAGCTCGTGAAGGCGAGATTCCATCTCCAGAGAACCGCAACACACTG 300
Db 235 TATCCAGAGCTCGTGAAGGCGAGATTCCATCTCCAGAGAACCGCAACACACTG 294

QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGCTTG 360
Db 295 TATCTGCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGACAG 354

QY 361 ACTCAGGCTGTGAC-----TCCTGGGCGCAGGAGTCTCGTCACTCTCTCA 411
Db 355 ACTACTATGACTTACTTTGCTTACTTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 411

RESULT 14
ID AAF69242 standard; DNA; 411 BP.
XX AAF69242;
XX


```
Qy 241 TACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 235 TATCCAGACAGTGTGAAGGGCGATTACCATCTCCAGAGACAATTCCAAGNACACGCTG 294
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 295 TATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGACAG 354
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 ACTACAGGGTCTGAC-----TCCTGGGGCCAGGGAGTCCCTGGTCACCGTCTCCTCA 411
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 ACTACTATGACTTACTTTGCTTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 411
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: July 15, 2003, 08:28:00
Job time : 157.369 secs

Software version 5.1.6
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EMBL/GenBank/TrEMBL search using sw-motif

Run on July 15, 2003, 08:48:23 : Search time 106.385 seconds
without alignment(s)
6100047 Million cell updates/sec

Total 411 sequences

Sequences 1-411 are kept in the database as they are significant

Sequences 1-411 are kept in the database as they are significant

Source 113441 seqs, 28940661 positions

Total number of hits satisfying chosen parameters: 2210862

Minimum IP seq length: 10

Maximum IP seq length: 2000000

IP seq length: 1000

IP seq length: 1000

IP seq length: 1000

Published Applications NA:
1. /usr2/6/prodat/1/pubna/US07 NEW PUB. seq.
2. /usr2/6/prodat/1/pubna/US07 NEW PUB. seq.
3. /usr2/6/prodat/1/pubna/US06 PUBCOMB. seq.
4. /usr2/6/prodat/1/pubna/US06 PUBCOMB. seq.
5. /usr2/6/prodat/1/pubna/US07 PUBCOMB. seq.
6. /usr2/6/prodat/1/pubna/US07 PUBCOMB. seq.
7. /usr2/6/prodat/1/pubna/US08 NEW PUB. seq.
8. /usr2/6/prodat/1/pubna/US08 PUBCOMB. seq.
9. /usr2/6/prodat/1/pubna/US09 NEW PUB. seq.
10. /usr2/6/prodat/1/pubna/US09 PUBCOMB. seq.
11. /usr2/6/prodat/1/pubna/US10 NEW PUB. seq.
12. /usr2/6/prodat/1/pubna/US10 PUBCOMB. seq.
13. /usr2/6/prodat/1/pubna/US10 PUBCOMB. seq.
14. /usr2/6/prodat/1/pubna/US10 PUBCOMB. seq.
15. /usr2/6/prodat/1/pubna/US10 PUBCOMB. seq.

Final Results are the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is followed by analysis of the final score distribution.

SUMMARIES

Seq. No.	Score	Match Length	DB	Description
1	41.8	411	US 10 101-686 4	Sequence 4, Appl
2	41.8	411	US 09 292-441 4	Sequence 4, Appl
3	41.8	411	US 09 441-441 4	Sequence 58, Appl
4	41.8	411	US 10 102-441 4	Sequence 58, Appl
5	41.8	411	US 10 103-441 4	Sequence 58, Appl
6	41.8	411	US 10 104-441 4	Sequence 58, Appl
7	41.8	411	US 10 105-441 4	Sequence 58, Appl
8	41.8	411	US 10 106-441 4	Sequence 58, Appl
9	41.8	411	US 10 107-441 4	Sequence 58, Appl
10	41.8	411	US 10 108-441 4	Sequence 58, Appl
11	41.8	411	US 10 109-441 4	Sequence 58, Appl
12	41.8	411	US 10 110-441 4	Sequence 58, Appl
13	41.8	411	US 10 111-441 4	Sequence 58, Appl
14	41.8	411	US 10 112-441 4	Sequence 58, Appl
15	41.8	411	US 10 113-441 4	Sequence 58, Appl
16	41.8	411	US 10 114-441 4	Sequence 58, Appl
17	41.8	411	US 10 115-441 4	Sequence 58, Appl
18	41.8	411	US 10 116-441 4	Sequence 58, Appl
19	41.8	411	US 10 117-441 4	Sequence 58, Appl
20	41.8	411	US 10 118-441 4	Sequence 58, Appl

20	256.4	62.4	1395	9	US-10 101-686 4	Sequence 4, Appl
21	256.4	62.4	1392	9	US-10 102-441 4	Sequence 4, Appl
22	256.4	62.4	1391	10	US-09 292-441 4	Sequence 4, Appl
23	256.4	62.4	407	9	US-09 441-441 4	Sequence 58, Appl
24	256.4	62.4	1392	9	US-10 102-441 4	Sequence 58, Appl
25	256.4	62.4	1798	9	US-09 441-441 4	Sequence 58, Appl
26	256.4	62.4	1798	10	US-09 441-441 4	Sequence 58, Appl
27	256.4	62.4	1413	9	US-10 103-441 4	Sequence 58, Appl
28	256.4	62.4	408	10	US-09 441-441 4	Sequence 58, Appl
29	256.4	62.4	397	9	US-10 104-441 4	Sequence 58, Appl
30	256.4	62.4	397	9	US-09 441-441 4	Sequence 58, Appl
31	256.4	62.4	397	9	US-10 105-441 4	Sequence 58, Appl
32	256.4	62.4	1678	10	US-09 441-441 4	Sequence 58, Appl
33	256.4	62.4	1708	10	US-10 106-441 4	Sequence 58, Appl
34	256.4	62.4	1720	9	US-10 107-441 4	Sequence 58, Appl
35	256.4	62.4	720	9	US-09 441-441 4	Sequence 58, Appl
36	256.4	62.4	720	10	US-09 441-441 4	Sequence 58, Appl
37	256.4	62.4	1617	10	US-09 441-441 4	Sequence 58, Appl
38	256.4	62.4	1565	10	US-09 441-441 4	Sequence 58, Appl
39	256.4	62.4	348	9	US-10 108-441 4	Sequence 58, Appl
40	256.4	62.4	423	10	US-09 441-441 4	Sequence 58, Appl
41	256.4	62.4	402	10	US-09 441-441 4	Sequence 58, Appl
42	256.4	62.4	348	9	US-10 109-441 4	Sequence 58, Appl
43	256.4	62.4	1654	9	US-09 441-441 4	Sequence 58, Appl
44	256.4	62.4	1654	9	US-09 441-441 4	Sequence 58, Appl
45	256.4	62.4	1590	10	US-09 441-441 4	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-10-101-686 4
Sequence 4, Application US/10103686
Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REEF, Mitchell E.
KLOETZER, William S.
NAXAGRA, William S.
TITLE OF INVENTION: GAMMA 1 ANT: HUMAN T-CELL RECEPTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DEANE, SWF KEE 5 VALLEY
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #10103686
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US10103686
FILING DATE: 25-Mar-2002
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US09001700
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,631
REFERENCE/DOCKET NUMBER: 010112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-6620
TELEFAX: (703) 816-6620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

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/
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..411
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 58..411
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-103-686-4

Query Match          99.2%; Score 407.8; DB 9; Length 411;
Best Local Similarity 99.5%; Pred. No. 1.2e-117;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGAGTTTGGCTGAGCTGGGTTTCTTGTCTCTTTGAAAGGTCTCCAGTGTGAG 60
Db 1 ATGGAGTTTGGCTGAGCTGGGTTTCTTGTCTCTTTGAAAGGTCTCCAGTGTGAG 60

QY 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTCTCC 120
Db 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTCTGG 120

QY 121 TCGCAGCCTCCGGTTGAGTTTCACTTCAATAAATACTACTGAGACTGGTCCGCCAG 180
Db 121 TCGCAGCCTCCGGTTGAGTTTCACTTCAATAAATACTACTGAGACTGGTCCGCCAG 180

QY 181 GCTCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCACATGG 240
Db 181 GCTCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCACATGG 240

QY 241 TACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCCAAACACACTG 300
Db 241 TACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCCAAACACTG 300

QY 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAGCTTG 360
Db 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAGCTTG 360

QY 361 ACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCGTCCCTCTCTCA 411
Db 361 ACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCGTCCCTCTCTCA 411
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RESULT 2

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US-09-019-441-4
/ Sequence 4: Application US/09019441
/ Publication No. US2003008621A1
/ GENERAL INFORMATION:
/ APPLICANT: REFF, Mitchell E.
/ NAKAMURA, Takehiko
/ KLOETZER, William S.
/ TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
/ ANTI-BODIES AND USE THEREOF AS THERAPEUTICS
/ NUMBER OF SEQUENCES: 35
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
/ STREET: P.O. Box 1404
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22313-1404
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/019,441
/ FILING DATE: 05-Feb-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/803,085
```

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/
/ FILING DATE: 20-FEB-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Teskin, Robin L.
/ REGISTRATION NUMBER: 35,030
/ REFERENCE/DOCKET NUMBER: 012712-532
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 836-6620
/ TELEFAX: (703) 836-2021
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 411 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..411
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 58..411
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-019-441-4
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Query Match 99.2%; Score 407.8; DB 9; Length 411;
Best Local Similarity 99.5%; Pred. No. 1.2e-117;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGGAGTTTGGCTGAGCTGGGTTTCTTGTCTCTTTGAAAGGTCTCCAGTGTGAG 60
Db 1 ATGGAGTTTGGCTGAGCTGGGTTTCTTGTCTCTTTGAAAGGTCTCCAGTGTGAG 60

QY 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTCTCC 120
Db 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTCTGG 120

QY 121 TCGCAGCCTCCGGTTGAGTTTCACTTCAATAAATACTACTGAGACTGGTCCGCCAG 180
Db 121 TCGCAGCCTCCGGTTGAGTTTCACTTCAATAAATACTACTGAGACTGGTCCGCCAG 180

QY 181 GCTCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCACATGG 240
Db 181 GCTCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCACATGG 240

QY 241 TACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCCAAACACACTG 300
Db 241 TACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAAAGCGCCAAACACTG 300

QY 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAGCTTG 360
Db 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACAGCGTGTCTATTACTGTGCGAGCTTG 360

QY 361 ACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCGTCCCTCTCTCA 411
Db 361 ACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCGTCCCTCTCTCA 411
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RESULT 3

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US-09-423-800-58
/ Sequence 58, Application US/09423800
/ Patent No. US20020165363A1
/ GENERAL INFORMATION:
/ APPLICANT: SATO, KOH
/ APPLICANT: TSUNENARI, TOSHIKI
/ APPLICANT: ISHII, KIMIE
/ TITLE OF INVENTION: CACHEXIA REMEDY
/ FILE REFERENCE: 04853-0036
/ CURRENT APPLICATION NUMBER: US/09/423,800
/ CURRENT FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: PCT/JP98/02116
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: JP 125505/1997
/ PRIOR FILING DATE: 1997-05-15
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Db 61 GTGCAGCTGGTGGAGTCTGGGGAGCGGTGGTTCAGCCTGGGAGGTCCCTGAGACTCTCC 120
Qy 121 TCGCAGACCTCCGGGTTCAGGTTTCACTTAATACTACTACAGACTGGGTCCGCCAG 180
Db 121 TGTGAGACCTCTG-----GATTCACCTTCAGTAGTATGGCATGTCTTGGGTCCGCCAG 174
Qy 181 GTCCAGGCGAGGGGTGGAGTGGGTCTCACGTATTAGTGTAGTGGTGTATCCCATATGG 240
Db 175 GCTCCAGGCAAGGGCTGGAGTGGGTGGCAACCATAGTGTGGTGTAGTTACACCTAC 234
Qy 241 TACGAGACTCCGTGAAGGGAGATTCACCATCTCCAGAGAGAAAGCCCAACACACTG 300
Db 235 TATCCAGACAGTGTGAAGGGGCGATTACCATCTCCAGAGACAATTTCCAAGAACACGCTG 294
Qy 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGCTTG 360
Db 295 TATCTGCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGAGAG 354
Qy 361 ACTCAGGGTCTGAC-----TCCTGGGGCCAGGGAGTCTCTGGTCACCGTCTCTCTCA 411
Db 355 ACTACTATGACTTACTTCTGCTTACTTGGGGCCAGGGAACCTGTCAACCGTCTCTCTCA 411
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RESULT 6

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US-10-125-237-73
; Sequence 73, Application US/10125237
; Publication No. US2003002329A1
```

GENERAL INFORMATION:

```
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chonghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US2003002329A1el Nucleic Acids and
; FILE REFERENCE: 79ICIP2ADIV
; CURRENT APPLICATION NUMBER: US/10/125,237
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 09/668,317
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/552,929
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 73
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(507)
```

US-10-125-237-73

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Query Match 65.3%; Score 268.4; DB 9; Length 690;
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Best Local Similarity 86.8%; Pred. No. 5e-74;
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Matches 309; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
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Qy 1 ATGGAGTTTGGCTGAGCTGGGTTTCTTGTCTCTTTTGAAGGTGTCCAGTGTGAG 60
Db 97 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTGTGTATTTTAAAGGTGTCCAGTGTGAG 156
Qy 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCTCCAGACTCTCC 120
Db 157 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGTAGTTCAGCCTGGGGGTCTCCAGACTCTCC 216
Qy 121 TCGCAGCCTCCGGTTCAGGTTTCACTTAATACTACTACAGACTGGGTCCGCCAG 180
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Db 217 TGTGAGCCTCTG-----GATTCACCTTCAGTAGTACTGATGCACTGGTCCGCCAA 270
Qy 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGTGATCCACATGG 240
Db 271 GCTCAGGGAAGGGCTGGTGGGTCTCAGTATTAAATAGTATGGAGTAGCACAAGC 330
Qy 241 TACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAAAGCCCAACACACTG 300
Db 331 TACCGGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAACGCCAAGACACGCTG 390
Qy 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGAG 356
Db 391 TATCTGCAATGAACAGTCTGAGAGCCGAGACACGGCTGTGTATTACTGTGCAAG 446
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RESULT 7

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US-10-105-891-73
; Sequence 73, Application US/10105891
; Publication No. US20030073099A1
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GENERAL INFORMATION:

```
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chonghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030073099A1el Nucleic Acids and
; FILE REFERENCE: 79ICIP2A
; CURRENT APPLICATION NUMBER: US/10/105,891
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE: 09/668,317
; PRIOR APPLICATION NUMBER: 2000-09-22
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 73
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(507)
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US-10-105-891-73

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Query Match 65.3%; Score 268.4; DB 9; Length 690;
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Best Local Similarity 86.8%; Pred. No. 5e-74;
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Matches 309; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
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Qy 1 ATGGAGTTTGGCTGAGCTGGGTTTCTTGTCTCTTTTGAAGGTGTCCAGTGTGAG 60
Db 97 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTGTGTATTTTAAAGGTGTCCAGTGTGAG 156
Qy 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCTCCAGACTCTCC 120
Db 157 GTGCAGCTGGTGGAGTCTGGGGCGGCTTAGTTCAGCCTGGGGGTCTCCAGACTCTCC 216
Qy 121 TCGCAGCCTCCGGTTCAGGTTTCACTTAATACTACTACAGACTGGGTCCGCCAG 180
Db 217 TGTGAGCCTCTG-----GATTCACCTTCAGTAGTACTGATGCACTGGGTCCGCCAA 270
Qy 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGTGATCCACATGG 240
Db 271 GCTCAGGGAAGGGCTGGTGGGTCTCAGTATTAAATAGTATGGAGTAGCACAAGC 330
Qy 241 TACCGAGCTCCGTGAAGGGCAGATTACCATCTCCAGAGAGAAAGCCCAACACACTG 300
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Db 100 ATGGAGTTTGGGCTGAGCTGGCTTTTCTTTGGCTATTTTAAAGGTCTCCAGTGTGAG 159
Qy 61 GTGCAGCTGGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120
Db 160 GTGCAGCTGTTGGAGTCTGGGGAGCTTGGTACAGCTGGGGGTCCCTGAGACTCTCC 219
Qy 121 TCGCAGCCTCCGGGTTACAGGTTTCACTTCAATAACTACTACATGAGTGGTCCGCCAG 180
Db 220 TGTGAGCCTCTG-----GATTACCTTTAGCAGTATGCCATGAGTGGTCCGCCAG 273
Qy 181 GCTCAGGCGCAGGGCTGGAGTGGGTCTCACGTTATAGTGGTGGTATCCCATATGG 240
Db 274 GCTCCAGGAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACATAC 333
Qy 241 TAGCAGACTCCGTGAAGGCGAGATTCCACATCTCCAGAGAAAGCCCAACACACTG 300
Db 334 TAGCAGACTCCGTGAAGGCGGTTCACATCTCCAGAGAAATTCCAAGAACACGCTG 393
Qy 301 TTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGA 355
Db 394 TATCTGCAATGAACAGCCTGAGAGCGGAGACAGCGCGGTATATTACTGTGCGA 448

RESULT 11

US-09-844-684-14
; Sequence 14, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:

; APPLICANT: GEMINI SCIENCE, INC.
; TITLE OF INVENTION: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; FILE REFERENCE: 21286/0276339
; CURRENT APPLICATION NUMBER: US/09/844,684
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-14

Query Match 64.3%; Score 264.2; DB 10; Length 630;
Best Local Similarity 86.2%; Pred. No. 1e-72;
Matches 306; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCTTTGTTCTCTTTTGAAGGTCTCCAGTGTGAG 60
Db 100 ATGGAGTTTGGGCTGAGCTGGCTTTTCTTTGGCTATTTTAAAGGTCTCCAGTGTGAG 159
Qy 61 GTGCAGCTGGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120
Db 160 GTGCAGCTGTTGGAGTCTGGGGAGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCC 219
Qy 121 TCGCAGCCTCCGGGTTACAGTTCACCTTCAATACTACTACATGAGTGGTCCGCCAG 180
Db 220 TGTGAGCCTCTG-----GATTACCTTTAGCAGTATGCCATGAGTGGTCCGCCAG 273
Qy 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTTATAGTGGTGGTATCCCATATGG 240
Db 274 GCTCCAGGAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGGTAGCACATAC 333
Qy 241 TAGCAGACTCCGTGAAGGCGAGATTCCACATCTCCAGAGAAAGCCCAACACACTG 300
Db 334 TAGCAGACTCCGTGAAGGCGGTTCACATCTCCAGAGAAATTCCAAGAACACGCTG 393
Qy 301 TTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGA 355
Db 394 TATCTGCAATGAACAGCCTGAGAGCGGAGACAGCGCGGTATATTACTGTGCGA 448

RESULT 12

US-10-040-244-12
; Sequence 12, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIYUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBODIES
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17

; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 12
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-12

Query Match 63.5%; Score 261; DB 9; Length 580;
Best Local Similarity 85.6%; Pred. No. 9.7e-72;
Matches 304; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

Qy 1 ATGCAGTTTGGGCTGAGCTGGGTTTTCTTTGTTCTCTTTTGAAGGTGTCCAGTGTGAG 60
Db 32 ATGCAGTTTGGGCTGGCTGGCTTTTCTTTGGCTATTTTAAAGGTGTCCAGTGTGAG 91
Qy 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
Db 92 GTGCAGCTGTTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCC 151
Qy 121 TGGCAGCCTCCGGGTTACAGTTCACCTTCAATACTACTACATGAGTGGTCCGCCAG 180
Db 152 TGTGAGCCTCTG-----GATTGCGCTTTAGCAGCTATGCCATGAGTGGTCCGCCAG 205
Qy 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGTATTTAGTAGTGTGATGCCACATGG 240
Db 206 GCTCAGGGAAGGGCTGGAGTGGGTCTCAGTATTTAGTAGTGTGTTGGTAGCACATAC 265
Qy 241 TAGCAGACTCCGTGAAGGCGAGATTCCCATCTCCAGAGAAAGCCCAACACACTG 300
Db 266 TAGCAGACTCCGTGAAGGCGCGTTCCACATCTCCAGAGACAATTCCAAGAACACGCTG 325
Qy 301 TTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGA 355
Db 326 TATCTGCAAAATGAACAGCCTGAGAGCGGAGACAGCGCGGTATATTACTGTGCGA 380

RESULT 13

US-09-844-684-12
; Sequence 12, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:

; APPLICANT: GEMINI SCIENCE, INC.
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339
; CURRENT APPLICATION NUMBER: US/09/844,684
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 580

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1  TYPE DNA
2  SEQUENCE: Homo sapiens
3  Length: 1427 base pairs
4  TYPE: nucleic acid
5  STRANDEDNESS: single
6  TOPOLOGY: linear
7  SEQUENCE DESCRIPTION: SEQ ID NO: 25:
8  US-10-066-895-25
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10 Query Match
11 Best Local Similarity 63.2% Score 263.6, DB 127, Domain 14.25
12 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 1
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; FILING DATE: 01-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Geiger, Kathleen
; REGISTRATION NUMBER: 35,880
; REFERENCE/DOCKET NUMBER: PS0504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5968
; TELEFAX: 610-270-5090
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-066-895-20

Query Match          62.8%; Score 258; DB 12; Length 1427;
Best Local Similarity 79.8%; Pred. No. 1.1e-70;
Matches 335; Conservative 0; Mismatches 70; Indels 15; Gaps 2;

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QY      61  GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGCTCCCTGAGACTCTCC 120
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QY      121  TCCGAGCCTCCGGGTTCAAGTTTCACTTCAATAACTACATGAGACTGGGTCCGCCAG 180
DB      133  TGTGCAGCCTCG-----GAACCACTCTAGTGGCTATACCATGCATCTGGGTCCGCCAG 186

QY      181  GCTCCAGGCGAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCCATATGG 240
DB      187  GCTCCAGGGAAGGGCTGGAGTGGGTCTCATCTTACTGGAGGTAGCAACTTCATAAAC 246

QY      241  TACGCAGACTCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
DB      247  TACTCAGACTCAGTGAAGGCCGATTACCATCTCCAGAGAACGCCAAGACTCACTT 306

QY      301  TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTCCGAGTTG 360
DB      307  TATCTGCAATGAACAGCCTGACAGCGAGGACACGGCTGTCTATTATTGTCCGACCGCC 366

QY      361  ACTACAG-----GGTCTGACTCTGGGGCCAGGGAGTCTCGTACCGTCTCTCTCA 411
DB      367  CCTATAGCACCGCCCTACTTTGACCACCTGGGGCCAGGGAAACCTGCTACCGTCTCTCTCA 426
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Job time : 109.385 secs

Genome version 5.1.6
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AM analysis: multiple search, using sw mode

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Search algorithm: Exhaustive alignment

4416.976 Million cell updates/sec

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85: /cgn2_6/prodata/1/pna/US042_1.MB.seq

Pred. No. is the number of results that satisfy the query.
Score greater than or equal to the score of the result. Results printed
and is derived by analysis of the total score distribution.

SUMMARIES

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1	411	100.0	411	16	US-09-292-053-7	Sequences: 100,000,000
2	407.8	99.2	411	16	US-09-292-053-7	Sequences: 100,000,000
3	407.8	99.2	411	16	US-09-292-053-7	Sequences: 100,000,000
4	285.8	69.5	1710	23	US-09-617-46A-1	Sequences: 100,000,000
5	285.8	69.5	1710	23	US-09-617-46A-1	Sequences: 100,000,000
6	285.8	69.5	1721	23	US-09-617-46A-1	Sequences: 100,000,000
7	285.8	69.5	1721	24	US-09-611-451A-1	Sequences: 100,000,000
8	280	68.1	1709	17	US-09-359-921-164	Sequences: 100,000,000
9	280	68.1	1709	17	US-09-359-921-164	Sequences: 100,000,000
10	280	68.1	1709	34	US-09-519-052-164	Sequences: 100,000,000
11	277.2	67.4	591	25	US-09-652-151-164	Sequences: 100,000,000
12	277.2	67.4	591	27	US-09-698-013-164	Sequences: 100,000,000
13	277.2	67.4	591	28	US-09-711-281-164	Sequences: 100,000,000
14	270.6	65.8	411	16	US-09-269-411-164	Sequences: 100,000,000
15	270.6	65.8	411	18	US-09-423-801-164	Sequences: 100,000,000
16	270.6	65.8	411	38	US-10-013-611-164	Sequences: 100,000,000
17	270.6	65.8	411	38	US-10-016-611-164	Sequences: 100,000,000
18	270.6	65.8	411	38	US-10-019-611-164	Sequences: 100,000,000
19	270.6	65.8	411	38	US-10-143-611-164	Sequences: 100,000,000
20	270.6	65.8	411	41	US-10-182-611-164	Sequences: 100,000,000
21	270.6	65.8	411	42	US-10-222-611-164	Sequences: 100,000,000

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22 269.2 65.5 1458 23 US-09-617-746A-193 Sequence 193, App
23 269.2 65.5 1458 24 US-09-631-451A-193 Sequence 193, App
24 269.2 65.5 1458 25 US-09-652-125A-9393 Sequence 9393, App
25 269.2 65.5 1458 26 US-09-652-127-9452 Sequence 9452, App
26 269.2 65.5 1458 27 US-09-652-916-10122 Sequence 10122, A
27 269.2 65.5 1458 28 US-09-699-999-7481 Sequence 7481, App
28 269.2 65.5 1458 29 US-09-710-281-5795 Sequence 7955, App
29 269.2 65.5 1458 30 US-09-716-475-7305 Sequence 7305, App
30 269.2 65.5 1458 31 US-09-726-175-3019 Sequence 3019, App
31 269.2 65.5 1458 32 US-09-726-176-1849 Sequence 1849, App
32 269.2 65.5 1458 33 US-09-726-211-1347 Sequence 1347, App
33 268.4 65.3 645 1. PCT-US01-08655-72 Sequence 72, Appl
34 268.4 65.3 690 26 US-09-668-317-73 Sequence 73, Appl
35 268.4 65.3 690 40 US-10-105-891-73 Sequence 73, Appl
36 268.4 65.3 690 40 US-10-125-237-73 Sequence 73, Appl
37 266.8 64.9 432 18 US-09-431-517-21418 Sequence 21418, A
38 266.6 64.9 1426 1. PCT-US02-20181-1 Sequence 1, Appl
39 265.4 64.6 1983 18 US-09-491-404-2415 Sequence 2415, App
40 265.4 64.6 1983 34 US-09-922-279-2415 Sequence 2415, App
41 265.4 64.6 1983 34 US-09-922-279A-2415 Sequence 2415, App
42 265.2 64.5 520 32 US-09-844-684-10 Sequence 10, Appl
43 265.2 64.5 520 38 US-10-040-244-10 Sequence 10, Appl
44 264.8 64.4 413 16 US-09-293-972-4372 Sequence 4372, App
45 264.8 64.4 413 34 US-09-904-939-4372 Sequence 4372, App
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ALIGNMENTS

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RESULT 1
US-09-292-053-7
; Sequence 7, Application US/09292053
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: NAKAMURA, TAKEHIKO
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
; FILE REFERENCE: 23522.0699
; CURRENT APPLICATION NUMBER: US/09/292,053
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 08/803,085
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 7
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
; NAME/KEY: CDS
; LOCATION: (1)..(411)
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US-09-292-053-7
Query Match 100.0%; Score 411; DB 16; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.9e-102;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGAGTTTGGGTGAGCTGGGTTTTCCTTTGTTTCTCTTTTCAAAGGTGTCAGTGTGAG 60

QY 61 GTGCAGCTGGTGAAGTCTGGGGCGGCTTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120
Db 61 GTGCAGCTGGTGAAGTCTGGGGCGGCTTTGGCAAGCCCTGGGGGTCCCTGAGACTCTCC 120

QY 121 TCGGCAGCTCCGGGTTTCAAGTTTCACTTCACTACTACTACTACTACTACTACTACTACTACT 180
Db 121 TCGGCAGCTCCGGGTTTCAAGTTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 180
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QY 181 GCTCCAGGCGAGGCGCTGGAGTGGGTCTCAGTATTAGTAGTGTGATCCACATGG 240
Db 181 GCTCCAGGCGAGGCGCTGGAGTGGGTCTCAGTATTAGTAGTGTGATCCACATGG 240

QY 241 TACCAGACTCCGTGAAGGCGAGATTCCCATCTCCAGAGAGAACGCCAACACACTG 300
Db 241 TACCAGACTCCGTGAAGGCGAGATTCCCATCTCCAGAGAGAACGCCAACACACTG 300

QY 301 TTTCTTCAATGACACGCTGAGAGCTGAGGACACGCTCTCTATTACTGTGCGAGCTTG 360
Db 301 TTTCTTCAATGACACGCTGAGAGCTGAGGACACGCTCTCTATTACTGTGCGAGCTTG 360

QY 361 ACTACAGGCTGACTCTCTGGGGCCAGGAGTCTCGTCCCGTCTCTCTCA 411
Db 361 ACTACAGGCTGACTCTCTGGGGCCAGGAGTCTCGTCCCGTCTCTCTCA 411
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RESULT 2

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US-09-019-441-4
; Sequence 4, Application US/09019441
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: NAKAMURA, TAKEHIKO
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,441
; FILING DATE: 05-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-502
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..411
; NAME/KEY: mat_peptide
; LOCATION: 58..411
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-019-441-4
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Query Match 99.2%; Score 407.8; DB 14; Length 411;
Best Local Similarity 99.5%; Pred. No. 3.7e-101;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359,922A
; EARLIER FILING DATE: 1999-07-22
; EARLIER FILING DATE: 1998-12-03
; EARLIER FILING DATE: 1998-12-03
; EARLIER FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-359-922-264

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Best Local Similarity 82.6%; Pred. No. 6e-66;
Matches 355; Conservative 0; Mismatches 50; Indels 25; Gaps 2;

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QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
Db 1486 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAGCCTGGGGGTCCCTGAGACTCTCC 1427

QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATTAACCTACTACATGAGTGGTCCGCCAG 180
Db 1426 TGTGAGCCTCTG-----GATTCACTTCAATGATTATGCCATGAGCTGGTCCGCCAG 1373

QY 181 GCTCAGGCGAGGGGCTGGAGTGGGTCTCAGGTATTTAGTAGTAGTGTGATCCACATGG 240
Db 1372 GCTCAGGCGAAGGGGCTGGAGTGGGTCTCAGGTATTTAGTAGTAGTGTGATCCACATAC 1313

QY 241 TAGCAGACTCCGTTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 1312 TACCCAGACTCTGTGAAGGCGCGATTCCCATCTCCAGAGAGAACGCCAACACTG 1253

QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 1252 TATCTGCAATGAACAGCCTGAGAGCGGAGGACACGGCTGTGTATTACTGTGCGAGAGGA 1193

QY 361 ACTACAGGG-----TCTGACTCTCTGGGCGCAGGAGTCTCTGTCAC 401
Db 1192 CCTCAGCGTGTGTGCTGCTCCCTTCCACATGACTCTCTGGGCGCAGGAAACCTGTGTCAC 1133

QY 402 CGTCTCCTCA 411
Db 1132 CGTCTCCTCA 1123

RESULT 10
US-09-919-002-264/c
; Sequence 284, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; EARLIER FILING DATE: 2001-07-30
; EARLIER FILING DATE: 1999-07-22
; EARLIER FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
```

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; SEQ ID NO 264
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-264

Query Match      68.1%; Score 280; DB 34; Length 1709;
Best Local Similarity 82.6%; Pred. No. 6e-66;
Matches 355; Conservative 0; Mismatches 50; Indels 25; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTTGTCTCTTTTGAAGGTGTCAGTGTGAG 60
Db 1546 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTTGTCTCTTTTGAAGGTGTCAGTGTGAG 1487

QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
Db 1486 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAGCCTGGGGGTCCCTGAGACTCTCC 1427

QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATTAACCTACTACATGAGTGGTCCGCCAG 180
Db 1426 TGTGAGCCTCTG-----GATTCACTTCAATGATTATGCCATGAGCTGGTCCGCCAG 1373

QY 181 GCTCAGGCGAGGGGCTGGAGTGGGTCTCAGGTATTTAGTAGTAGTGTGATCCACATGG 240
Db 1372 GCTCAGGCGAAGGGGCTGGAGTGGGTCTCAGGTATTTAGTAGTAGTGTGATCCACATAC 1313

QY 241 TAGCAGACTCCGTTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 1312 TACCCAGACTCTGTGAAGGCGCGATTCCCATCTCCAGAGAGAACGCCAACACTG 1253

QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 1252 TATCTGCAATGAACAGCCTGAGAGCGGAGGACACGGCTGTGTATTACTGTGCGAGAGGA 1193

QY 361 ACTACAGGG-----TCTGACTCTCTGGGCGCAGGAGTCTCTGTCAC 401
Db 1192 CCTCAGCGTGTGTGCTGCTCCCTTCCACATGACTCTCTGGGCGCAGGAAACCTGTGTCAC 1133

QY 402 CGTCTCCTCA 411
Db 1132 CGTCTCCTCA 1123

RESULT 11
US-09-652-127-9891
; Sequence 9891, Application US/09652127
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; LIBRARIES
; FILE REFERENCE: 1600.1183-001
; CURRENT APPLICATION NUMBER: US/09/652,127
; EARLIER FILING DATE: 2000-08-30
; EARLIER FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10475
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9891
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-127-9891

Query Match      67.4%; Score 277.2; DB 25; Length 591;
Best Local Similarity 82.6%; Pred. No. 2.7e-65;
Matches 347; Conservative 0; Mismatches 58; Indels 15; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTTGTCTCTTTTGAAGGTGTCAGTGTGAG 60
Db 96 ATGGAAGTGGGGCTCCGCTGGGTTTCTTGTCTCTTTTGAAGGTGTCAGTGTGAG 155

QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
```


;; PRIOR FILING DATE: 1996-09-26
;; PRIOR APPLICATION NUMBER: JP 214168/1997
;; PRIOR FILING DATE: 1997-07-24
;; NUMBER OF SEQ ID NOS: 113
;; SOFTWARE: PatentIn ver. 2.1
;; SEQ ID NO 58
;; LENGTH: 411
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(411)
;; NAME/KEY: sig_peptide
;; LOCATION: (1)..(57)
;; NAME/KEY: mat_peptide
;; LOCATION: (58)..(411)
US-09-269-332-58

Query Match 65.8%; Score 270.6; DB 16; Length 411;
Best Local Similarity 81.8%; Pred. No. 1.6e-63;
Matches 341; Conservative 0; Mismatches 64; Indels 12; Gaps 2;

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Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60
Db 1 ATGGGTTTGGGCTGAGCTGGGTTTCCCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60

Qy 61 GTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTCC 120
Db 61 GTGCAGCTGGTGGAGTCTGGGGGAGCGTGGTCCAGCTGGGAGGTCCTGAGACTCTCC 120

Qy 121 TGCAGCTCCCGGTTTCAGGTTTCACTTCAATAACTACTACATGAGCTGGGTCCGCCAG 180
Db 121 TGTGAGCCTCTG-----GATTTCACCTTCAGTAGCTATGGCATGTCTTGGTCCGCCAG 174

Qy 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTAGTGGTATCCACATGG 240
Db 175 GCTCAGGCGAAGGGGCTGGAGTGGGTGGCAACCATTTAGTGGTGTAGTTACACCTAC 234

Qy 241 TACGAGACTCCGTGAAGGCGAGATTCCACATCTCCAGAGAGAACGCCAACACACATG 300
Db 235 TATCCAGACAGTGTGAAGGGCGGATTCCACATCTCCAGAGACAAATTCAGAACACGCTG 294

Qy 301 TTTCTTCAAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGTTG 360
Db 295 TATCTGCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGACAG 354

Qy 361 ACTACAGGTTCTGAC-----TCCTGGGCGCAGGAGTCTCGTCCCGTCTCTCA 411
Db 355 ACTACTATGACTTACTTTGCTTACTTGGGCGCAGGAAACCTGGTCAACCGTCTCTCA 411
```

RESULT 15

US-09-423-800-58
; Sequence 58, Application US/09423800
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 411
; TYPE: DNA

;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(411)
;; NAME/KEY: sig_peptide
;; LOCATION: (1)..(57)
;; NAME/KEY: mat_peptide
;; LOCATION: (58)..(411)
US-09-423-800-58

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Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60
Db 1 ATGGGTTTGGGCTGAGCTGGGTTTCCCTTGTTCCTTTTGAAGGTTCCAGTGTGAG 60

Qy 61 GTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTCC 120
Db 61 GTGCAGCTGGTGGAGTCTGGGGGAGCGTGGTCCAGCTGGGAGGTCCTGAGACTCTCC 120

Qy 121 TGCAGCTCCCGGTTTCAGGTTTCACTTCAATAACTACTACATGAGCTGGGTCCGCCAG 180
Db 121 TGTGAGCCTCTG-----GATTTCACCTTCAGTAGCTATGGCATGTCTTGGTCCGCCAG 174

Qy 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTAGTGGTATCCACATGG 240
Db 175 GCTCAGGCGAAGGGGCTGGAGTGGGTGGCAACCATTTAGTGGTGTAGTTACACCTAC 234

Qy 241 TACGAGACTCCGTGAAGGCGAGATTCCACATCTCCAGAGAGAACGCCAACACACATG 300
Db 235 TATCCAGACAGTGTGAAGGGCGGATTCCACATCTCCAGAGACAAATTCAGAACACGCTG 294

Qy 301 TTTCTTCAAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGTTG 360
Db 295 TATCTGCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGACAG 354

Qy 361 ACTACAGGTTCTGAC-----TCCTGGGCGCAGGAGTCTCGTCCCGTCTCTCA 411
Db 355 ACTACTATGACTTACTTTGCTTACTTGGGCGCAGGAAACCTGGTCAACCGTCTCTCA 411
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Search completed: July 15, 2003, 11:46:01
Job time : 1613.85 secs


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QY 121 TGGCAGCTCCGGGTTCAAGTTCACTTCAATAAATACTACTACATGAGTGGTCCGCCAG 180
Db 121 TGTGACGCTCTG-----GATTACCTTCAGTAGTTTCTAGGATGAATGGGTCCGCCAG 174
QY 181 GCTCCAGGCGAGGGCTGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCATGG 240
Db 175 GTCTCCAGGCGAGGGCTGAGTGGGTCTCATCTATTACTAGTAGTATTACATATAC 234
QY 241 TACGCAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 TACGCAGACTCAGTGAAGGCGGATTACCATCTCCAGAGAGAACGCCAAGAACTCACTG 294
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTCCGAGCTTG 360
Db 295 TATCTGCAATGAACAGCTGAGAGCGGAGGACAGCGCTGTCTATTACTGTCCGAGATT 354
QY 361 A---CTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGGTCAACGCTCTCTCA 411
Db 355 ACAGCTATGGCCCTTGACTACTTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 408

RESULT 2
US-10-309-762-112
; Sequence 112, Application US/10309762
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Hands, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-112

Query Match 69.3%; Score 284.8; DB 14; Length 408;
Best Local Similarity 84.1%; Pred. No. 3.1e-75;
Matches 348; Conservative 0; Mismatches 57; Indels 9; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGAGGTTTCTTCTTCTCTCTTTTGAAGGTGTCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTGCGCTGGGTTTCTTCTTCTTCTTCTTATTTAGAAAGGTGTCAGTGTGAG 60
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGCTTGGCAAGCCTGGGGGTCTCCAGACTCTCC 120
Db 61 GTGCAGTTGGTGGAGTTTGGGGAGGCTGGTCAAGCCTGGAGGTTCTCCAGACTCTCC 120
QY 121 TGGCAGCTCGGTGGAGTCTGGGGCGCTTGGCAAGCCTGGGGGTCTCCAGACTCTCC 180
Db 121 TGGCAGCTCTG-----GATTCACTTCAATACTACTACATGAGTGGTCCGCCAG 174
QY 181 GCTCCAGGCGAGGGCTGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCATGG 240
Db 175 GCTCCAGGGAAGGGCTGGAGTGGGTTTCATACATTAGTCTTAGTGGCAGTACCATATAC 234
QY 241 TACGCAGCTCCGGGTTCAAGTTCACTTCAATAAATACTACTACATGAGTGGTCCGCCAG 300
Db 235 TACGCAGCTCTG-----GATTCACTTCAATAAATACTACTACATGAGTGGTCCGCCAG 294
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTCCGAGCTTG 360
Db 295 TATCTGCAATGAACAGCTGAGAGCGGAGGACAGCGCTGTCTATTACTGTCCGAGATT 354
QY 361 A---CTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGGTCAACGCTCTCTCA 411
Db 355 ACAGCTATGGCCCTTGACTACTTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 408
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Db 355 ACAGCTATGGCCCTTGACTACTTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 408

RESULT 3
PCT-US02-38540-126
; Sequence 126, Application PC/TUS0238540
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: FOLTZ, Ian
; APPLICANT: BASCOCK, John
; APPLICANT: PALATHUMPAT, Raju
; APPLICANT: YANG, Xiao-dong
; APPLICANT: KING, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; FILE REFERENCE: ABGENIX.029VPC
; CURRENT APPLICATION NUMBER: PCT/US02/38540
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38540-126

Query Match 68.6%; Score 282; DB 2; Length 414;
Best Local Similarity 83.3%; Pred. No. 2.2e-74;
Matches 350; Conservative 0; Mismatches 55; Indels 15; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTTCTCTCTTTTGAAGGTGTCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTTAGCTGGGTTTCTCTTCTCTTATATAAAGGTGTCAGTGTGAG 60
QY 61 GTGCAGCTGTGTGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCTCCAGACTCTCC 120
Db 61 GTGCACCTGTGTGAGTCTGGGGAGGCTTGGTCAAGCCTGGAGGTTCTCCAGACTCTCC 120
QY 121 TGGCAGCTCCGGGTTCAAGTTCACTTCAATAAATACTACTACATGAGTGGTCCGCCAG 180
Db 121 TGGCAGCTCTG-----GATTCACTTCAATAAATACTACTACATGAGTGGTCCGCCAG 174
QY 181 GCTCCAGGCGAGGGCTGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCATGG 240
Db 175 GCTCCAGGGAAGGGCTGGAGTGGGTTTCATACATTAGTCTTAGTGGCAGTACCATATAC 234
QY 241 TACGCAGACTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 TACGCAGACTCTGTGAAGGCGGATTCAACATCTCCAGGAGAACGCCAAGAACTCACTG 294
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTCCGAGCTTG 360
Db 295 TTTCTGCAATGAACAGCTGAGAGCGGAGGACAGCGCTGTATTACTGTGCGAGAGG 354
QY 361 AC-----TACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTGGTCAACGCTCTCTCA 411
Db 355 GCGGCTAGGCTGACTACTTTTGACTACTTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 414

RESULT 4
US-10-309-764-126
; Sequence 126, Application US/10309764
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; FILE REFERENCE: ABGENIX.029VPC
; CURRENT APPLICATION NUMBER: PCT/US02/38540
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38540-126
```


Db 175 GTCCAGGAGGAGGCTGGAGTGGGTTTCATACATTAGTAGTAGTGTCCCAATTTAC 234
Qy 241 TAGCGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAAACGCCAACACACTG 300
Db 235 TAGCGAGACTCTGTGAAGGCGGATTACCATCTCCAGGACAATGCCAAGAACTACTG 294
Qy 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 295 TATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCGGTGATTACTGTGCGAAGG 354
Qy 361 ACT-----ACAGGCTGACTCTCTGGGCGCAGGAGTCTCGGTACCGTCTCTCTCA 411
Db 355 ACTGGATCTACGACGCTCTTTGACTACTGTGGGCCAGGGAACCTGTGACCGTCTCTCA 414

RESULT 7

PCT-US03-18934-94
; Sequence 94, Application PC/TUS0318934
; GENERAL INFORMATION:
; APPLICANT: diadexus, Inc.
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Peptides
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: PCT/US03/18934
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/389,327
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 1493
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US03-18934-94

Query Match 67.2%; Score 276.2; DB 1; Length 1493;
Best Local Similarity 81.8%; Pred. No. 1.9e-72; Mismatches 68; Indels 6; Gaps 1;
Matches 333; Conservative 0;
Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTTTGTTCTCTTTTCAAGGTGTCAGTGTGAG 60
Db 68 ATGGAGTTTGGGCTGAGCTGGCTTTTCTTTGGCTATTTTTAAAGGTGTCAGTGTGAG 127
Qy 61 GTGCAGCTGGTGGAGTCTGGGGGCGCTTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
Db 128 GTGCAGCTGTGGAGTCTGGGGGAGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCC 187
Qy 121 TCGCAGCCTCCGGGTTTCAGGTTTCACTTCAATACTACTACATGAGCTGGGTCCGCCAG 180
Db 189 TGTGAGCCTCTG-----GATTCACCTTTAGCATCTATGCCATGAGCTGGGTCCGCCAG 241
Qy 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTTATTAGTAGTAGTGGGTGATCCCACTGG 240
Db 242 GCTCCAGGGAAGGGCTGGAGTGGGTCCGAAGTATCAGTTTCAGTGGTGTAGTACATAC 301
Qy 241 TAGCGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAAACGCCAACACACTG 300
Db 302 TAGCGAGACTCCGTGAAGGCGGTTTACCATCTCCAGAGACAATTCGAAGACCACTGATG 361
Qy 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 362 CATCTCCACATGAACAGCCTGAGAACCGAGACACGGCGGTCTACTACTGTGCGAACC 421
Qy 361 ACTACAGGCTGACTCTCTGGGGCCAGGAGTCTGGTCAACGCTCTC 407
Db 422 TTTCCGTATTTTGTACTACTGTGGGCCAGGGAACCTTGGTCAACGCTCTC 468

RESULT 8

PCT-US02-38540-94
; Sequence 94, Application PC/TUS0238540
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; FILE REFERENCE: ABGENIX.029A
; CURRENT APPLICATION NUMBER: PCT/US02/38540
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38540-94

Query Match 66.6%; Score 273.8; DB 2; Length 405;
Best Local Similarity 81.0%; Pred. No. 6.5e-72;
Matches 333; Conservative 0; Mismatches 72; Indels 6; Gaps 1;
Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTTTTGAAGGTGTCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTGCGCTGGGTTTCTCTCTTTTAAAGAGGTGTCAGTGTGAG 60
Qy 61 GTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCTGGGGGTCCCTCAGACTCTCC 120
Db 61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGTCCAGCCTGGGAGTCTCTGAGAGTCTCC 120
Qy 121 TCGCAGCCTCCGGGTTTTCAGTTTCACTTCAATACTACTACATGAGCTGGGTCCGCCAG 180
Db 121 TGTGAGCGCTG-----GATTCACCTTTCAGTAACTATGTCATGCTGGGTCCGCCAG 174
Qy 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTATCCACATGG 240
Db 175 GCTCCAGCAAGGGCTGGAGTGGGTGGCGATTATATGGTATGATGAAGTAAATAATTC 234
Qy 241 TACGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAAACGCCAACACACTG 300
Db 235 TATCGAGACTCCGTGAAGGCGCGATTACCATCTCCAGAGACAATTCAGAGAACCGCTG 294
Qy 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 295 TCTCTCAATGAGCAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGC 354
Qy 361 ACTACAGGCTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCTCTCA 411
Db 355 GGTGGGACTTTGACTTTCTGGGGCCAGGAAACCTGTGTCACCGTCTCTCTCA 405

RESULT 9

US-10-309-764-94
; Sequence 94, Application US/10309764
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
; FILE REFERENCE: ABGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-03

QY 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATCCCATGG 240
DB 175 GCTCAGGCGAAGGGCTGGAGTGGGTGGCAATTATATGTATGATGGAGTAAAAATTC 234
QY 241 TAGCAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
DB 235 TATGCAGACTCCGTGAAGGCGGATTACCATCTCCAGAGACAAATTCACAAACACGCTG 294
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
DB 295 TATCTGCAGCTGAACAGCCTGAGAGTCGAGGACACGGCTGTCTATTACTGTGCGAGAGG 354
QY 361 ACTCAGGCTCTGACTCTCGGGCCAGGAGTCTTGCTGCTCAGCTCTCTCA 411
DB 355 GCGGCTGACATTGACTTCTGGGGCCAGGGAACCTGGTCACCGTCTCTCTCA 405

RESULT 12
PCT-US02-38540-134
; Sequence 134, Application PC/TUS0238540
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: FOLTZ, Ian
; APPLICANT: BABCOOK, John
; APPLICANT: PALATHUMPAT, Raju
; APPLICANT: YANG, Xiao-dong
; APPLICANT: KING, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR4SRB ANTIBODIES FOR USE IN
; TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: ABGENIX.029VPC
; CURRENT APPLICATION NUMBER: PCT/US02/38540
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-38540-134

Query Match 66.3%; Score 272.4; DB 2; Length 414;
Best Local Similarity 81.9%; Pred. No. 1.7e-71;
Matches 344; Conservative 0; Mismatches 61; Indels 15; Gaps 2;
QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
DB 1 ATGGAGTTTGGGCTGCTGCTGGGTTTCTTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
DB 61 GTGCAGCTGGTGGAGTCTGGGGGAGACTTGGTCAAGCCTGGAGGTCCCTGAGACTCTCC 120
QY 121 TGCAGAGCTCCGGGTTACAGTTTCAATTAATCTACATGAGTGGGTCCGCCAG 180
DB 121 TGTGAGCTCTGGATTGAG-----CTTCAGTGGCTACTTCTGAGCTGGATCCGCCAG 174
QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATCCCATGG 240
DB 121 TGTGAGCTCTGGATTGAG-----CTTCAGTGGCTACTTCTGAGCTGGATCCGCCAG 174
QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATCCCATGG 240
DB 175 GCTCCAGGGAAGGGCTGGAGTGGGTCTCAACTATTAGTGGTGGTAGCACATAC 234
QY 241 TAGCAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
DB 235 TATGCAGACTCCGTGAAGGCGGATTACCATCTCCAGAGACAAATTCACAAACACGCTG 294
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
DB 295 CATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCGTGTATTACTGTGCGAGAGG 354
QY 361 ACT-----ACAGGCTCTGACTCTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCTCTCA 411
DB 355 GCGGCTGACATTGACTTCTGGGGCCAGGGAACCTGGTCACCGTCTCTCTCA 405

DB 355 ACTGAACTACGAGGTCTTTGACTACTGGGGCCAGGGAACCTGGTACCGTCTCTCTCA 414
RESULT 13
PCT-US03-09260-5
; Sequence 5, Application PC/TUS0309260
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation and Abgenix, Inc.
; APPLICANT: Greenfeder, Scott
; APPLICANT: Corvalan, Jose
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COM
; FILE REFERENCE: LI01564WI
; CURRENT APPLICATION NUMBER: PCT/US03/09260
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-09260-5

Query Match 66.3%; Score 272.4; DB 2; Length 414;
Best Local Similarity 81.9%; Pred. No. 1.7e-71;
Matches 344; Conservative 0; Mismatches 61; Indels 15; Gaps 2;
QY 1 ATGCAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
DB 1 ATGCAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
DB 61 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCTGGGGGTCCCTGAGACTCTCC 120
QY 121 TGCAGCCTCCGGGTTTCACTTCAATTAATCTACATGAGTGGGTCCGCCAG 180
DB 121 TGTGAGCTCTGGATTGAG-----GATTACCTTTAGCAGCTATGCCATGAGTGGGTCCGCCAG 174
QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTATCCCATGG 240
DB 175 GCTCCAGGGAAGGGCTGGAGTGGGTCTCAACTATTAGTGGTGGTAGCACATAC 234
QY 241 TAGCAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
DB 235 TATGCAGACTCCGTGAAGGCGGTTTCACTCTCCAGAGACAAATTCACAAACACGCTG 294
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
DB 295 TATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCGCTATATTACTGTGCGAAAGAG 354
QY 361 A-----CTACAGGCTGAGTCTCTGGGGCCAGGAGTCCCTGGTACCGTCTCTCTCA 411
DB 355 AGGTATAACTGGAACCTACCTACACTACTGGGGCCAGGGAACCTGGTACCGTCTCTCTCA 414

RESULT 14
US-10-309-764-134
; Sequence 134, Application US/10309764
; GENERAL INFORMATION:
; APPLICANT: Foltz, Ian
; APPLICANT: Babcock, John
; APPLICANT: Palathumpat, Raju
; APPLICANT: Yang, Xiao-dong
; APPLICANT: King, Chadwick T.
; TITLE OF INVENTION: ANTI-CDR4SRB ANTIBODIES FOR USE IN
; TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
; FILE REFERENCE: ABGENIX.029A
; CURRENT APPLICATION NUMBER: US/10/309,764
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337,276
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 147


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Db 232 TATGCAGACTCCGTGAAGGCCGCGATTCCACATCTCCAGAGAAAATGCCAAGAACTCCTTG 291
Qy 301 TTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTGTGCGAGCTTG 360
Db 292 TATCTTACAAATGAACGCGCTGAGAGCGCGGAGACAGCGCTGTGTATTACTGTGCAAG---- 347
Qy 361 ACTACAGGCTGTGACTCTCTGGGCGCAGGAGTCTGTGTCACCGTCTCTCTCA 411
Db 348 -----AGATTAGAACTCTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 393

RESULT 5
US-08-468-671-3
; Sequence 3, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,671
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,372
; FILING DATE: 14-JUN-1994
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOHETICAL: NO
; ANTI-SENSE: NO
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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Hybridoma
; CELL LINE: ZM1-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..393
US-08-468-671-3

Query Match 62.1%; Score 255.4; DB 1; Length 393;
Best Local Similarity 82.0%; Pred. No. 2.7e-67;
Matches 337; Conservative 0; Mismatches 56; Indels 18; Gaps 3;

Qy 1 ATGGAGTTTGGCTGAGCTGGGTTTCTCTTCTTCTCTTTTGAAGGTGTCCAGTGTGAG 60
Db 1 ATGGAGTTTGGCTGAGCTGGGTTTCTCTTCTTCTCTTTTGAAGGTGTCCAGTGTGAG 60

Qy 61 GTGCAGCTGTGGAGTCTGGGGGCGGTTGCAAGCCTGGGGGTCCCTGAGACTCTCC 120
Db 61 GTGCAGCTGTGGAGTCTGGGGGAGGTTTGGTACAGCCTGGGGGTCCCTGAGACTCTCC 120

Qy 121 TGGCAGCCTCCGGGTTTCAGGTTTCCCTTCAATTAATACTACATGAGTGGTCCGCCAG 180
Db 121 TGTGAGCCTCTG-----GATTCACTTCACTAGGTACGACATGTACTGGTCCGCCAA 174

Qy 181 GCTCAGGCGCAGGCGCTGGGTTCTCAGTATTAGTAGTGTGATCCACATGG 240
Db 175 GCTACAGGAAAGGTCTGGAGTGGTCTCAGTATTGGTCTCTACTGTGA---CACATAC 231

Qy 241 TACGCACTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACTG 300
Db 232 TATGCAGACTCCGTGAAGGCGGATTCAACATCTCCAGAGAAAATGCCAAGAACTCCTTG 291

Qy 301 TTTCTTCAATGAACAGCTGTGAGCTGAGACAGCGCTGTCTATTACTGTGCGAGCTTG 360
Db 292 TATCTTCAATGAACGCGCTGAGAGCGGCGGACAGCGCTGTGTATTACTGTGCAAG---- 347

Qy 361 ACTACAGGCTGTGACTCTCTGGGCGCAGGAGTCTCTGTGTCACCGTCTCTCTCA 411
Db 348 -----AGATTAGAACTCTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 393

RESULT 6
US-08-259-372A-1
; Sequence 1, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
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1 PRI-P APPLICATION DATA:
2 APPLICATION NUMBER: US 07/530,134
3 FILING DATE: 16 JUN 1992
4 PRI-P APPLICATION DATA:
5 APPLICATION NUMBER: US 07/132,764
6 FILING DATE: 15 MAY 1988
7 PRI-P APPLICATION DATA:
8 APPLICATION NUMBER: US 06/025,196
9 FILING DATE: 15 OCT 1986
10 PRI-P APPLICATION DATA:
11 APPLICATION NUMBER: US 06/194,611
12 FILING DATE: 25 SEP 1986
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Smith, William M.
15 PUBLICATION NUMBER: 1,192,351
16 PUBLICATION DATE: 1992
17 PUBLICATION INFORMATION:
18 TELEPHONE: (415) 576-0300
19 TELEFAX: (415) 576-0300
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 423 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: cDNA
26 HYPOTHETICAL: NO
27 ANTI-SENSE: NO
28 ORIGINAL SOURCE:
29 ORGANISM: Homo sapiens
30 CELL TYPE: Hybridoma
31 CELL LINE: P81.1
32 FEATURE:
33 NAME/KEY: CDS
34 LOCATION: 1..423
35 US-09-468-671-1
36
37 Query Match 59.6%; Score 249; E-12; Length 423;
38 Best Local Similarity 92.8%; E-04; N-1; Gap 64;
39 Matches 234; Conservative
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Db 61 GTCCAGCTGGTGGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGTCCCTGAGACTCTCC 120
Qy 121 TCGCAGCCTCCGGGTTCAGGTTTCACTTCAATACTACTACATGACTGGGTCCGCCAG 180
Db 121 TGTGAGCCTCTG-----GATTCACTTCAGTAGTATGGCATGCACTGGGTCCGCCAG 174
Qy 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGATCCCATATGG 240
Db 175 GCTCCAGGCAAGGGCTGGAGTGGGTGGCAGTGATATCATATGATGAAGTAATAATGG 234
Qy 241 TAGCAGACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 TATGAGACTCCGTGAAGGCGGATTCACCATCTCCAGAGACAATTCGAAGAACACTG 294
Qy 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACAGGCTGTCTATTACTGTGCGA 355
Db 295 TTCTGCAATGCACAGCCTGAGAGCTGCGGACAGGCTGTATATTACTGTGCGA 349

RESULT 8

US-08-545-809A-21
; Sequence 21, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiro
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
US-08-545-809A-21

Query Match 58.2%; Score 239, 4; DB 3; Length 519;
Best Local Similarity 85.6%; Pred. No. 1.8e-62;
Matches 280; Conservative 0; Mismatches 41; Indels 6; Gaps 1;
Qy 30 TGTCTCTCTTTTAAAGGTGTCCAGTGTGAGGTGCGAGTGTGGGGGGCGGCTT 89

Db 141 TGTCTCTCTCTTTTCCAGGTGTCCAGTGTGAGTGCACACTGGTGGAGTCTGGGGAGGCGCT 200
Qy 90 GGCAAGCCTGGGGGTCCCTGAGACTCTCTCGCGAGCCTCCGGGTTCAGGTTCACTT 149
Db 201 GGTCAAGCCTGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTG-----GATTCACTT 254
Qy 150 CAATAACTACTACATGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTC 209
Db 255 CAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAGAGGGGCTGGAGTGGGTCTC 314
Qy 210 ACGTATTAGTAGTAGTGGTGTATCCCATGATGTCAGCAGACTCTCGTGAAGGCGAGATTAC 269
Db 315 ATCCATTAGTAGTAGTAGTTACATATATACATGACAGACTCTAGTGAAGGCCGATTAC 374
Qy 270 CATCTCCAGAGAGAACGCCAACACACTGTTTCTTCAATGAACAGCCTGAGAGCTGA 329
Db 375 CATCTCCAGAGAGAACGCCAACACTCACTGTATCTGCAATGAACAGCCTGAGAGCGGA 434
Qy 330 GGACACGGCTGTCTATTACTGTGCGAG 356
Db 435 GGACACGGCTGTATTACTGTGCGAG 461

RESULT 9

US-08-545-809A-48
; Sequence 48, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiro
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
US-08-545-809A-48

Query Match 58.1% Score 10.9 DB 3 Length 743
 Best Local Similarity 85.6% Pct. Nucleotide 62
 Matches 280 Conservative 0 Mismatches 41 Indels 6 Gaps 1

QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 89
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 89
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 149
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 149
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 419
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 419
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 209
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 209
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 479
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 479
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 269
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 269
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 539
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 539
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 329
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 329
 QV 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 599
 DB 10 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 599

RESULT 1
 US-08-134-346A-49
 Sequence 49, Application US/08134346A
 Patent No. 628135
 GENERAL INFORMATION:
 APPLICANT: de Courtois, F.J.R.
 APPLICANT: Ceriani, R.L.C.
 APPLICANT: Petersen, J.A.
 TITLE OF INVENTION: HYPERIDOMA AND ANTI-H4 HEMANGIOMA
 TITLE OF INVENTION: MONOCLONAL ANTIBODY AND ASSAYS FOR DETECTING AND TREATING HEMANGIOMA
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Ostlager, Chomel & Flabiaty
 STREET: 300 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10022-7499
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, also incl. 1.44 MB floppy
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/134,346A
 FILING DATE: 08-OCT-1993
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Chofrio, Dara L.
 REGISTRATION NUMBER: 34,899
 REFERENCE/DOCKET NUMBER: 149,439
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-826-6564
 TELEFAX: 212-826-6389
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 417 base pairs
 TYPE: nucleic acid

ORGANISM: Homo sapiens
 CELL TYPE: human lymphoblast
 CELL LINE: CGM1
 US-08-545-809A-11

Query Match 58.1% Score 10.9 DB 3 Length 743
 Best Local Similarity 85.4% Pct. Nucleotide 62
 Matches 280 Conservative 0 Mismatches 41 Indels 6 Gaps 1

QV 29 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 89
 DB 29 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 89
 QV 331 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 149
 DB 331 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 149
 QV 89 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 209
 DB 89 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 209
 QV 391 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 479
 DB 391 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 479
 QV 149 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 269
 DB 149 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 269
 QV 445 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 539
 DB 445 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 539
 QV 209 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 329
 DB 209 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 329
 QV 505 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 599
 DB 505 TTTTCTTTTAAATTTTCAATTTATTTTACCTGCTGAGCTGCTGGGGGCGCTT 599

RESULT 11
 US-08-134-346A-49
 Sequence 49, Application US/08134346A
 Patent No. 628135
 GENERAL INFORMATION:
 APPLICANT: de Courtois, F.J.R.
 APPLICANT: Ceriani, R.L.C.
 APPLICANT: Petersen, J.A.
 TITLE OF INVENTION: HYPERIDOMA AND ANTI-H4 HEMANGIOMA
 TITLE OF INVENTION: MONOCLONAL ANTIBODY AND ASSAYS FOR DETECTING AND TREATING HEMANGIOMA
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Ostlager, Chomel & Flabiaty
 STREET: 300 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10022-7499
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, also incl. 1.44 MB floppy
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/134,346A
 FILING DATE: 08-OCT-1993
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Chofrio, Dara L.
 REGISTRATION NUMBER: 34,899
 REFERENCE/DOCKET NUMBER: 149,439
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-826-6564
 TELEFAX: 212-826-6389
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 417 base pairs
 TYPE: nucleic acid

```
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-134-346A-49

Query Match      57.2%; Score 235; DB 4; Length 417;
Best Local Similarity 76.6%; Pred. No. 3.5e-61;
Matches 321; Conservative 0; Mismatches 80; Indels 18; Gaps 2;

QY 1 ATGGAGTTTGGCTGAGCTGGCTTTCTCTTTTGAAGGTTCCAGGTGAG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGACTTTGGCTGAGCTGGCTTTCTCTTTTGAAGGTTCCAGGTGAA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 GTGCAGCTGGTGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGCTCCCTGAGACTCTCC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GTGCAGATGGTGAGTCTGGGGGAGGCTTAGTGACGCTGGAGGCTCCCTGAGACTCTCC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 TCGCAGCTCCGGGTTCAAGTTCACTTCAATACTACTACATGAGCTGGTCCGCCAG 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 TGTGAGCCTCTG-----GATTGCTTTCACTAGCTATGCCATGTCTTGGGTTGCCAG 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 181 GCTCAGGCGAGGGCTGAGTGGTCTCAGCTATTAGTAGTGGTATCCCATGG 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 GTCCAGGGAAGGGCTGAGTGGTGGCGAGAAATTAGTGGTAAATTACGCCCTAC 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 241 TACGCAGACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAAAGCCCAACACACTG 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 TATCAAGACACTGTGAGCGGCGGATTCACCATCTCCAGAGACAAATCCAGAACACCTG 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGCGA----- 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 TACCTCAATGAACAGCTGAGGCTGAGGACAGCGCGGTGTATTACTGTCAAGGGAG 354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 356 -----GCTTGACTACAGGCTGACTCTCTGGGCGGAGTCTGGTACCGCTCTC 407
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 GACTACGGTATCCCGCCCTGGTTGCTTACTGGGGCCAGGGAGCTGTGTACTCTCTC 413
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-08-545-809A-23
; Sequence 23, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906

; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
US-08-545-809A-23

Query Match      56.2%; Score 230.8; DB 3; Length 514;
Best Local Similarity 85.0%; Pred. No. 6.9e-60;
Matches 272; Conservative 0; Mismatches 42; Indels 6; Gaps 1;

QY 36 TCTTTTGAAGGTTCCAGTGTGAGGTGCGAGTCTCGGAGTCTGGGGCGGCTTTGGCAAA 95
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 TTCTGTTTGCAGGTGTCAGTGTGAGGTGCAGCTGTTGAGTCTGGGGGAGGCTTGGTACA 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 96 GCCTGGGGGTCCTTGAGACTCTCTCGCGAGCCTCCGGGTTACGGTTTCACTTCAATAA 155
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 GCCTGGGGGTCCTTGAGACTCTCTCGCGAGCCTCTCTGTGAGCCTCTG-----GATTCACTTTAGCAG 261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 156 CTACTACATGAGTGGGTCCGCCAGGCTCCAGGCGAGGCTGGAGTGGGTCTCACGTAT 215
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 262 CTATGCCATGAGTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCAGCTAT 321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 216 TAGTAGTAGTGGTGAATCCCATGTTACGCAGACTCCGTGAAGGGCAGATTTCACCATCTC 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 322 TAGTGGTAGTGGTAGGACATACATACGCAGACTCCGTGAAGGGCGGTTACCATCTC 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 276 CAGAGAGAACCCCAACACACTGTTTCTTCAATGAACAGCCTGAGAGCTGAGGACAC 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 382 CAGAGACAATTCCAAAGAACAGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACAC 441
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 336 GGCTGTCTATTACTGTGCGA 355
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 442 GGCCGTATATTACTGTGCGA 461
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-08-619-491-7
; Sequence 7, Application US/08619491
; Patent No. 6210670
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,491
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/07302
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,963
```


1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Townsend and Townsend Khourie and Crew
3 STREET: 379 Lytton Avenue
4 CITY: Palo Alto
5 STATE: California
6 COUNTRY: US
7 ZIP: 94301
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: PatentIn Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/305,683A
15 FILING DATE: 13-SEP-1994
16 CLASSIFICATION: 424
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 07/759,279
19 FILING DATE: 13-SEP-1991
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Liebeschuetz, Joe
22 REGISTRATION NUMBER: 37,505
23 REFERENCE/DOCKET NUMBER: 11823-005230
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (415) 326-2400
26 TELEFAX: (415) 326-2422
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 426 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: cDNA
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: 1..426
37 OTHER INFORMATION: /product= "HSV863 heavy chain"
38 OTHER INFORMATION: variable region"
39 US-08-305-683A-1

Query Match 55.8%; Score 228.4; DB 1; Length 426;
Best Local Similarity 79.8%; Pred. No. 3.3e-59;
Matches 284; Conservative 0; Mismatches 66; Indels 6; Gaps 1;

Qy 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTTTTGAAGGTTCCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTTTTGAAGGTTCCAGTGTGAG 60

Qy 61 GTGACGCTGGTGGAGTCTCGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTTCC 120
Db 61 GTGACGCTGGTGGAGTCTCGGGCGGAGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTTCC 120

Qy 121 TCGGAGCCTCCGGGTTGAGTTTACCTTCAATACTACTACATGAGACTGGGTCCGCCAG 180
Db 121 TGTGCAGCGTCTG-----GATTACCTTCAGTAGCCATGTCTCATTTGGGTCCGCCAG 174

Qy 181 GCTCCAGGCGAGGGGCTGGAGTGGGTCTCACGTTATTAGTAGTGGTGTATCCCATGG 240
Db 175 GCTCCAGGCGAGGGGCTGGAGTGGGTCTCACGTTATTAGTAGTGGTGTATCCCATGG 234

Qy 241 TAGCGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGACGCCAACACACTG 300
Db 235 TATGGAGAGTCCGTGAAGGCGGATTTCATCATCTCCAGAGACAAATCCAAAGATATCCITG 294

Qy 301 TTCTTCAATGACAGCTGAGAGCTGAGGACACGGCTGTCTATTAATGTCGGAG 356
Db 295 TATCTGCAATGAACAGCTGAGAGCGGAGCACGGCTGTGTATTAATGTCGGAG 350

Search completed: July 15, 2003, 08:30:16
Job time : 33.4004 secs